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OM protein - protein search, using sw model

Run on: February 19, 2003, 16:21:10 ; Search time 82 Seconds  
(without alignments)  
705.253 Million cell updates/sec

Title: US-09-994-064-11

Sequence: 1 MRRPHLRKRSRYAKGEVLN.....ACAVLVGLVMSYKCAHS 434

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq.101002.\*

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22:	/SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23:	/SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2311	100.0	434	15	AA58856
2	2311	100.0	434	16	AA00638
3	2311	100.0	434	17	AA006790
4	2311	100.0	434	20	AA221984
5	2311	100.0	434	21	AA36040
6	2311	100.0	434	21	AA58184
7	197	8.5	393	10	AA90887
8	190	8.2	369	11	AA06489
9	190	8.2	369	20	AA081601
10	190	8.2	394	5	AA40083

11	189	8.2	394	6	AA50582	Sequence encoded b
12	184.5	8.0	442	13	AA21777	EHV-1 envelope gly
13	179	7.7	388	18	AA11333	HSV glycoprotein D
14	169	7.3	435	12	AA11273	HSV-1 antigen/heat
15	165.5	7.2	308	18	AA11322	HSV glycoprotein D
16	165.5	7.2	405	12	AA11272	HSV-1 antigen/heat
17	165	7.1	402	22	AA878824	Pseudorabies virus
18	165	7.1	402	22	AA004969	Pseudorabies virus
19	165	7.1	402	22	AA882501	Pseudorabies virus
20	165	7.1	973	12	AA14680	HSV surface antigen
21	164	7.1	402	15	AA63142	Glycoprotein 50 (g
22	162.5	7.0	373	17	AA96590	Protein encoded fr
23	162.5	7.0	373	21	AA32473	DNA encoding fell
24	162.5	7.0	374	22	AA50118	Feline herpesvirus
25	162	7.0	402	8	AA70644	Pseudorabies virus
26	161	7.0	402	21	AA076751	Novel recombinant
27	159	6.9	393	5	AA40084	Sequence of Herpes
28	159	6.9	393	18	AA11324	HSV glycoprotein D
29	158.5	6.9	394	6	AA50581	Sequence encoded b
30	158	6.8	393	19	AA72163	HSV-2 strain SB5 C
31	158	6.8	400	19	AA72143	HSV-2 strain SB5 C
32	158	6.8	400	19	AA72013	HSV-2 strain SB5 C
33	157	6.8	368	16	AA12068	HSV antigen gD2.
34	156.5	6.8	393	10	AA90748	Herpes simplex vir
35	156	6.8	402	22	AA05395	Pseudorabies virus
36	151.5	6.6	398	13	AA22322	Marx Disease Virus
37	148.5	6.4	417	14	AA37683	gIV from BHV-1 str
38	147.5	6.4	417	14	AA37684	gIV from BHV-1 str
39	144	6.2	417	14	AA37895	Sequence of a reco
40	144	6.2	417	14	AA41345	Bovine herpesvirus
41	144	6.2	417	16	AA77401	BHV1 gIV glycoprot
42	144	6.2	417	19	AA75800	Bovine herpes virus
43	144	6.2	417	21	AA96087	Bovine herpesvirus
44	143	6.2	300	22	AA50119	Feline herpesvirus
45	142.5	6.2	418	21	AA50086	Bovine herpesvirus

## ALIGNMENTS

RESULT 1					
ID	AA58856	AA58856 standard; Protein; 434 AA.			
XX	AA58856:				
AC	AA58856:				
XX					
DT	13-APR-1995 (first entry)				
XX					
DE	Product of gd gene of infectious laryngotracheitis virus (ILT).				
XX					
KW	Homology vector 586-36.6; gd gene; cassette gene.				
XX					
OS	Infectious laryngotracheitis virus.				
XX					
PN	W09419014-A.				
XX					
PD	01-SEP-1994.				
XX					
PF	28-FEB-1994; 94MO-US01826.				
XX					
PR	26-FEB-1993; 93US-0024156.				
XX					
PA	(JAPG ) NIPPON ZEON KK.				
XX	(SYTR ) SYNTRON CORP.				
PI	Cochran MD;				
XX					
DR	WPI; 1994-294007/36.				
XX	N-PSDB; AA068944.				
PT	New recombinant fowl pox virus for use in vaccines - contains				
PT	genes expressing antigens of Newcastle disease virus and opt.				
PT	Infectious bronchitis virus				

XX Disclosure; Page 76-77; 85pp; English.  
 PS  
 CC AA068944 contains the coding region of the ILT gd gene and was  
 CC derived from an approx. 2060 bp EcoRI to BclI restriction sub-  
 CC fragment of the ILT Kpni genomic restriction fragment #8 (10.6kb).  
 CC It is part of a cassette in plasmid 586-36.6 constructed for  
 CC the purpose of inserting ILT gb and gd genes into the fowlpox  
 CC virus (FPV).  
 CC  
 XX Sequence 434 AA;

Query Match 100.0%; Score 2311; DB 15; Length 434;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-204;  
 Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRPHLRHSRYAKGEVYLNKHMDCGKRCGSAVFTLFWTCVRIMEHCIFVNNAMDR 60  
 Db 1 MHRPHLRHSRYAKGEVYLNKHMDCGKRCGSAVFTLFWTCVRIMEHCIFVNNAMDR 60  
 QY 61 HLFNRNAFWTIVLLSSFSASOSTAAVTYDYLIGRRALDALITPAVGPNRYLTRVSRGCDV 120  
 Db 61 HLFNRNAFWTIVLLSSFSASOSTAAVTYDYLIGRRALDALITPAVGPNRYLTRVSRGCDV 120  
 QY 121 VELNPISNVDDMISAKEKEKGPEASVWVFYIKGDDGDKCPIYRKREYRCGCVOL 180  
 Db 121 VELNPISNVDDMISAKEKEKGPEASVWVFYIKGDDGDKCPIYRKREYRCGCVOL 180  
 QY 181 LSECASOAMWADVVPSTLVSRNGAGLTIFSPALSGOYLTLKIGRFAOTALTLE 240  
 Db 181 LSECASOAMWADVVPSTLVSRNGAGLTIFSPALSGOYLTLKIGRFAOTALTLE 240  
 QY 241 VNDRLKIGSQLNPLPSKWTTEQYQTFQGEHLIYPIADNTNRHADVYRGYEDIIQRMN 300  
 Db 241 VNDRLKIGSQLNPLPSKWTTEQYQTFQGEHLIYPIADNTNRHADVYRGYEDIIQRMN 300  
 QY 301 NLRRKNPSAPDRPDSVPOEIPAVTKKAGRTPDASSEKKAPEDESDDMAEASGEN 360  
 Db 301 NLRRKNPSAPDRPDSVPOEIPAVTKKAGRTPDASSEKKAPEDESDDMAEASGEN 360  
 QY 361 PALPPEDEVPEDEHDDPNSDPDYNDMPAVIPVEETTKSSNAVSMPIFAAFVACAVAL 420  
 Db 361 PALPPEDEVPEDEHDDPNSDPDYNDMPAVIPVEETTKSSNAVSMPIFAAFVACAVAL 420  
 QY 421 VGLLWMSIVKARS 434  
 Db 421 VGLLWMSIVKARS 434

RESULT 2

ID AA000638  
 AA000638 standard; Protein; 434 AA.

XX  
 AC AA000638;  
 XX  
 DT 19-NOV-1996 (first entry)  
 XX  
 DE Infectious laryngotracheitis virus glycoprotein gd.  
 XX  
 KM Infectious laryngotracheitis virus; ILTV; herpesvirus;  
 KM attenuation; vector; vaccine; chicken; poultry; immunisation;  
 KM glycoprotein gd.  
 XX  
 OS Infectious laryngotracheitis virus.  
 XX  
 PN W09508622-A1.  
 XX  
 PD 30-MAR-1995.  
 XX  
 PF 16-SEP-1994; 94WO-US10628.  
 XX  
 PR 24-SEP-1993; 93US-0126597.  
 XX

PA (SYTR ) SYNTRO CORP.  
 XX  
 PI Cochran MD, Wild MA;  
 XX  
 DR WPI; 1995-139591/18.  
 XX  
 DR N-PSDB; AAT33505.  
 XX  
 PT Recombinant attenuated infectious laryngotracheitis virus - for use  
 PT in vaccines to protect poultry from infection from the virus; also  
 PT methods of distinguishing between vaccinated and naturally infected  
 PT birds

Example 1; Page 108-109; 177pp; English.

CC Glycoprotein gd (AA000638) of infectious laryngotracheitis virus  
 CC (ILTV) is the product of the gd gene (AAT33505) that spans bases  
 CC 8462-9766 of the unique short region (see also AAT33504) of ILTV  
 CC genomic DNA. It has a mol.wt. of approx. 48,477 mol.wt. and is  
 CC homologous to pseudorabies virus g50 and to gd from herpes simplex  
 CC virus-1. Marek's disease virus, IPV and bovine herpesvirus-1.1.  
 CC Monoclonal antibodies raised to ILTV react specifically with gd  
 CC from ILTV and also with ILTV gd expressed in herpesvirus of  
 CC turkeys (HVT) virus vector. ILTV gd expressed in the HVT  
 CC vector is useful as a subunit vaccine.

Sequence 434 AA;

Query Match 100.0%; Score 2311; DB 16; Length 434;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-204;  
 Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRPHLRHSRYAKGEVYLNKHMDCGKRCGSAVFTLFWTCVRIMEHCIFVNNAMDR 60  
 Db 1 MHRPHLRHSRYAKGEVYLNKHMDCGKRCGSAVFTLFWTCVRIMEHCIFVNNAMDR 60  
 QY 61 HLFNRNAFWTIVLLSSFSASOSTAAVTYDYLIGRRALDALITPAVGPNRYLTRVSRGCDV 120  
 Db 61 HLFNRNAFWTIVLLSSFSASOSTAAVTYDYLIGRRALDALITPAVGPNRYLTRVSRGCDV 120  
 QY 121 VELNPISNVDDMISAKEKEKGPEASVWVFYIKGDDGDKCPIYRKREYRCGCVOL 180  
 Db 121 VELNPISNVDDMISAKEKEKGPEASVWVFYIKGDDGDKCPIYRKREYRCGCVOL 180  
 QY 181 LSECASOAMWADVVPSTLVSRNGAGLTIFSPALSGOYLTLKIGRFAOTALTLE 240  
 Db 181 LSECASOAMWADVVPSTLVSRNGAGLTIFSPALSGOYLTLKIGRFAOTALTLE 240  
 QY 241 VNDRLKIGSQLNPLPSKWTTEQYQTFQGEHLIYPIADNTNRHADVYRGYEDIIQRMN 300  
 Db 241 VNDRLKIGSQLNPLPSKWTTEQYQTFQGEHLIYPIADNTNRHADVYRGYEDIIQRMN 300  
 QY 301 NLRRKNPSAPDRPDSVPOEIPAVTKKAGRTPDASSEKKAPEDESDDMAEASGEN 360  
 Db 301 NLRRKNPSAPDRPDSVPOEIPAVTKKAGRTPDASSEKKAPEDESDDMAEASGEN 360  
 QY 361 PALPPEDEVPEDEHDDPNSDPDYNDMPAVIPVEETTKSSNAVSMPIFAAFVACAVAL 420  
 Db 361 PALPPEDEVPEDEHDDPNSDPDYNDMPAVIPVEETTKSSNAVSMPIFAAFVACAVAL 420  
 QY 421 VGLLWMSIVKARS 434  
 Db 421 VGLLWMSIVKARS 434

RESULT 3

ID AA006790  
 AA006790 standard; Protein; 434 AA.

XX  
 AC AA006790;  
 XX  
 DT 02-JUN-1997 (first entry)  
 XX  
 DE ILTV glycoprotein gd.

```

XX ILTV: vaccine; vector: attenuation; poultry;
KM avian infectious bronchitis virus; Newcastle disease virus;
KM infectious bursal disease virus of chickens;
KM Marek's disease virus; herpesvirus; glycoprotein gD.
XX
OS Infectious laryngotracheitis virus USDA strain 8302.
XX
FH Key Location/Qualifiers
FT Region 352..372
FT Modified-site /label=transmembrane_helix
FT 250..252
FT /label=glycosylation
FT /note="potential glycosylation site, but may not
FT be glycosylated owing to proline residue"
XX
PN WO629396-A1.
XX
PD 26-SEP-1996.
XX
PF 21-MAR-1996; 96WO-US03916.
XX
XX 06-JUN-1995; 95US-0468190.
XX PR 23-MAR-1995; 95US-0410121.
XX
XX (SYTR ) SYNTRO CORP.
XX
PI Cochran MD, Wild MA;
XX
PI WPI; 1996-443172/44.
XX
DR N-PSDB; AAT44384;
XX N-PSDB; AAT44385.
XX
PT Recombinant infectious laryngotracheitis virus with deletion in the
PT glycoprotein G, gI or US2 gene, etc. - useful for vaccines against
PT infectious laryngotracheitis in poultry
XX
XX Example 11; Page 116-117; 216pp; English.
XX
XX Glycoprotein gD (AAW06790) is encoded by ORF7 of the unique short
XX region (AA74384) of infectious laryngotracheitis virus (ILTV). It
XX shows homology to pseudorabies virus 950, and the gD from herpes
XX simplex virus-1, Marek's disease virus, IPV and bovine herpesvirus
XX 1.1. Expression of gD in vectored fowlpox virus or herpesvirus of
XX turkeys (HVT) is sufficient to raise a protective immune response
XX in chickens. ILTV gD expressed in a HVT vector is useful as a
XX subunit vaccine.
XX
SQ Sequence 434 AA:

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```

QY 301 NLTKKMPASDPDPDSVPOEIPAVTKKAGRPDAESSKKAPPEDEDDMOAEASGEN 360
DB 301 NLTKKMPASDPDPDSVPOEIPAVTKKAGCRTPDASSKKAPPEDEDDMOAEASGEN 360
QY 361 PAALPEDEVEPEDTEHDDPNSDPDYNDMPAVIPVEETTKSSNAVSPFPAFVACAVAL 420
DB 361 PAALPEDEVEPEDTEHDDPNSDPDYNDMPAVIPVEETTKSSNAVSPFPAFVACAVAL 420
QY 421 VGLLWMSIVKCAAS 434
DB 421 VGLLWMSIVKCAAS 434

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RESULT 4  
AA71964  
ID AAY21984 standard; Protein; 434 AA.  
XX  
AC AAY21984;  
XX  
DT 07-SEP-1999 (first entry)  
XX  
DE Seq ID No: 20 of US5925358.  
XX  
XX Fowlpox virus; FPV; recombinant; vaccine; immunisation; chicken; NDV;  
KM Newcastle disease virus; NDV; Fowlpox; Infectious laryngotracheitis.  
XX  
XX Fowlpox virus.  
XX  
OS US5925358-A.  
XX  
PN 20-JUL-1999.  
XX  
PD 07-JUN-1995; 95US-0484575.  
XX  
PF 07-JUN-1995; 95US-0484575.  
XX  
PR 07-JUN-1995; 95US-0484575.  
XX 26-FEB-1993; 93US-0024156.  
XX 28-FEB-1994; 94WO-US02252.  
XX  
XX (SYTR ) SYNTRO CORP.  
XX  
PI Cochran MD, Junker DE;  
XX  
PI WPI; 1999-418249/35.  
XX N-PSDB; AAX81152.  
XX  
PT Fowlpox viruses, useful as vaccines for immunization of  
PT chickens/turkeys against Fowlpox and Newcastle disease virus  
XX  
XX Disclosure; Column 77-82; 108pp; English.  
XX  
PS  
XX  
XX The invention relates to a recombinant fowlpox virus (FPV) comprising  
XX a foreign DNA inserted into a region of the fowlpox virus genome  
XX corresponding to a 2.8 kb EcoRI fragment, capable of being expressed in a  
XX host cell. The virus is used as a vaccine for immunising chickens against  
XX Newcastle disease virus (NDV), Fowlpox, and Infectious laryngotracheitis.  
XX  
SQ Sequence 434 AA:

Query Match 100.0%; Score 2311; DB 20; Length 434;  
Best Local Similarity 100.0%; Pred. No. 3.8e-204;  
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MHRPHLRHSRYAAKGEVLNKHMDCGKRCSCGAAVFTLFWTCVRIMREHICFVRNAMDR 60
DB 1 MHRPHLRHSRYAAKGEVLNKHMDCGKRCSCGAAVFTLFWTCVRIMREHICFVRNAMDR 60
QY 61 HLELRNAFWTIYLLSSFASQSTAAVYDYTLGRRALDALTIIPAVGPNRYLRFVSGCDV 120
DB 61 HLELRNAFWTIYLLSSFASQSTAAVYDYTLGRRALDALTIIPAVGPNRYLRFVSGCDV 120
QY 121 VELNPIISNVDMDISAAKEKEKGFPEASVYVFWIKGDGEDKXCPITYRKEYRECGDYOL 180
DB 121 VELNPIISNVDMDISAAKEKEKGFPEASVYVFWIKGDGEDKXCPITYRKEYRECGDYOL 180
QY 181 LSCCAVOSQOMAVDVPSTVSRNGAGLTIFSPALSSQYLLTLKIGFPAQTALVTLLE 240
DB 181 LSCCAVOSQOMAVDVPSTVSRNGAGLTIFSPALSSQYLLTLKIGFPAQTALVTLLE 240
QY 241 VNDRCIKISQNLNPLPSKMTTEQYOTGFGGELHLYPIADNTRHADVYRGYEDIIQRRN 300
DB 241 VNDRCIKISQNLNPLPSKMTTEQYOTGFGGELHLYPIADNTRHADVYRGYEDIIQRRN 300

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Db 121 VELNPISNVDDMI SAKEREKGGPF EASVWFYVIKGDGDEKXCPYRKEYRECGDVQL 180  
 QY 181 LSECAVQSAQMAVADVVPSTLVSRNGAGLTIPSPALSGOYLTLKIGRFAQTALVTL 240  
 Db 181 LSECAVQSAQMAVADVVPSTLVSRNGAGLTIPSPALSGOYLTLKIGRFAQTALVTL 240  
 QY 241 VNDRLCKIGSOLNPLPSKCMWTEQYOTGFQGHLYPIADTNTRHADVDYRGYEDILLQRMN 300  
 Db 241 VNDRLCKIGSOLNPLPSKCMWTEQYOTGFQGHLYPIADTNTRHADVDYRGYEDILLQRMN 300  
 QY 301 NLLRRKNPSAPDP RPDSPVQEIIPAVTKAEGRTPDASESEKKAPPESEDDMOAASGEN 360  
 Db 301 NLLRRKNPSAPDP RPDSPVQEIIPAVTKAEGRTPDASESEKKAPPESEDDMOAASGEN 360  
 QY 361 PALPEDDEVPEDETHDDPNSDPDYNDMPAVIPEETTKSSNAVSMPIFAAFVACAVAL 420  
 Db 361 PALPEDDEVPEDETHDDPNSDPDYNDMPAVIPEETTKSSNAVSMPIFAAFVACAVAL 420  
 QY 421 VGLVMSIVKCAR 434  
 Db 421 VGLVMSIVKCAR 434

RESULT 5  
 AAB36040  
 ID AAB36040 standard; Protein: 434 AA.

AC AAB36040;  
 DT 02-MAR-2001 (first entry)

DE Recombinant fowlpox virus-related polypeptide, SEQ ID NO: 20.

KM Fowlpox virus; FPV, antiviral; antibacterial; vaccine;  
 KW Newcastle's disease; Marek's disease; infectious laryngotracheitis.

OS Unidentified.

PN US6136318-A.

PD 24-OCT-2000.

PF 07-JUN-1995; 95US-0486414.

PR 26-FEB-1993; 93US-0024156.

PR 28-FEB-1994; 94WO-US02252.

PA (JUNK/) JUNKER D. E.  
 (COCH/) COCHRAN M. D.

PI Cochran MD, Junker DE;

PN WPI; 2000-686071/67.

PT New recombinant fowlpox virus useful as vaccines contains foreign DNA  
 inserted into specific non-essential region of the genome

PS Disclosure; Column 79-82; 56pp; English.

CC The present sequence is provided in a specification relating to a  
 CC recombinant fowlpox virus (FPV) that comprises a foreign DNA inserted  
 CC within a 3.5 kb EcoRI fragment of the FPV genomic DNA. The foreign DNA  
 CC can be expressed in host cells infected with FPV. The recombinant FPV  
 CC may be used in vaccines to protect animals (especially chickens) against  
 CC fowlpox and, depending on the source of the foreign DNA, other diseases,  
 CC particularly Newcastle's disease, Marek's disease or infectious  
 CC laryngotracheitis.

SO Sequence 434 AA;

Query Match 100.0%; Score 2311; DB 21; Length 434;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-204;  
 Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRPHLRHRRSYRYAKGEVLNKHMDCCGKRCCGAAYFTLFTGVRIMREHICFVRNADR 60  
 Db 1 MHRPHLRHRRSYRYAKGEVLNKHMDCCGKRCCGAAYFTLFTGVRIMREHICFVRNADR 60  
 QY 61 HFLRNAFWTIVLLSSFAQSOSTAATYDYLIGRRALDALITPAVGPNRYNLTIRVSGCDV 120  
 Db 61 HFLRNAFWTIVLLSSFAQSOSTAATYDYLIGRRALDALITPAVGPNRYNLTIRVSGCDV 120  
 QY 121 VELNPISNVDDMI SAKEREKGGPF EASVWFYVIKGDGDEKXCPYRKEYRECGDVQL 180  
 Db 121 VELNPISNVDDMI SAKEREKGGPF EASVWFYVIKGDGDEKXCPYRKEYRECGDVQL 180  
 QY 181 LSECAVQSAQMAVADVVPSTLVSRNGAGLTIPSPALSGOYLTLKIGRFAQTALVTL 240  
 Db 181 LSECAVQSAQMAVADVVPSTLVSRNGAGLTIPSPALSGOYLTLKIGRFAQTALVTL 240  
 QY 241 VNDRLCKIGSOLNPLPSKCMWTEQYOTGFQGHLYPIADTNTRHADVDYRGYEDILLQRMN 300  
 Db 241 VNDRLCKIGSOLNPLPSKCMWTEQYOTGFQGHLYPIADTNTRHADVDYRGYEDILLQRMN 300  
 QY 301 NLLRRKNPSAPDP RPDSPVQEIIPAVTKAEGRTPDASESEKKAPPESEDDMOAASGEN 360  
 Db 301 NLLRRKNPSAPDP RPDSPVQEIIPAVTKAEGRTPDASESEKKAPPESEDDMOAASGEN 360  
 QY 361 PALPEDDEVPEDETHDDPNSDPDYNDMPAVIPEETTKSSNAVSMPIFAAFVACAVAL 420  
 Db 361 PALPEDDEVPEDETHDDPNSDPDYNDMPAVIPEETTKSSNAVSMPIFAAFVACAVAL 420  
 QY 421 VGLVMSIVKCAR 434  
 Db 421 VGLVMSIVKCAR 434

RESULT 6  
 AAY38184

ID AAY38184 standard; Protein: 434 AA.

AC AAY38184;

DT 14-MAR-2000 (first entry)

DE ILTV glycoprotein D (9D).

FW Fowlpox virus; FPV; recombinant; antigenic protein; expression;

KW infectious laryngotracheitis virus; ILTV; Newcastle disease virus; NDV;  
 KW Marek's disease virus; cytokine; promoter; homologous recombination;

KW homology vector; multivalent; live vaccine; glycoprotein D.

OS Infectious laryngotracheitis virus.

PN US6001369-A.

PD 14-DEC-1999.

PF 07-JUN-1995; 95US-0477459.

PR 26-FEB-1993; 93US-0024156.

PR 28-FEB-1994; 94WO-US02252.

PA (SYTR ) SYNTRO CORP.

PI Junker DE, Cochran MD;

PN WPI; 2000-071638/06.

DR N-PSDB; AA49300.

PT Recombinant fowlpox virus useful as a vaccine for immunizing fowl  
 PT against Marek's disease, Newcastle disease, infectious  
 PT laryngotracheitis virus and/or fowlpox  
 PS Claim 5; Columns 79-80; 56pp; English.



CC The invention relates to a recombinant fowlpox virus (FPV)  
 CC comprising a foreign DNA inserted into a 4.2 kb EcoRI fragment  
 CC of the fowlpox virus genome. The foreign DNA is capable of being  
 CC expressed in a host cell into which the fowlpox virus has been  
 CC introduced and encodes an antigenic protein. The antigenic protein  
 CC which may be expressed includes infectious laryngotracheitis virus  
 CC (ILTAV) glycoprotein B (gB) or glycoprotein D (gD). AAY58184, Newcastle  
 CC disease virus (NDV) haemagglutinin (HN, AAY58182) or fusion (F) protein  
 CC (AAY58183) and Marek's disease virus gB or gD. The foreign DNA may  
 CC alternatively encode a cytokine such as chicken myelomonocytic growth  
 CC factor (CMGF) or chicken interferon (cIFN). The foreign DNA in the  
 CC recombinant FPV is under the control of one or more synthetic pox  
 CC promoters, enabling control of strength and timing of heterologous  
 CC gene expression. The synthetic pox virus promoters that may be used are  
 CC based on promoters of the vaccinia virus and include early promoter 1  
 CC (EPI), late promoter 1 (LPI), EPI2 and LP2 (AAZ49291-249294,  
 CC respectively). The recombinant FPV is generated via homologous  
 CC recombination between FPV DNA and a homology vector containing the  
 CC foreign DNA flanked by FPV sequences. The recombinant fowlpox viruses of  
 CC the invention are used as multivalent live vaccines for immunising fowl  
 CC against Marek's disease virus, NDV, ILTV and/or fowlpox virus. The  
 CC present sequence represents ILTV glycoprotein D (gD).

SO Sequence 434 AA:

Query Match 100.0%; Score 2311; DB 21; Length 434;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-204;

Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRPHLRHRSRYAKGEVLNKHMDGCGKCCSGAAVFTLFWTCVRIREHICFYRANMDR 60  
 DB 1 MHRPHLRHRSRYAKGEVLNKHMDGCGKCCSGAAVFTLFWTCVRIREHICFYRANMDR 60  
 QY 61 HLELRNAFWTIVLLSFAASQSTAAYTYDILGRRALDALTIPAVGPNRYLTRYSGCDV 120  
 DB 61 HLELRNAFWTIVLLSFAASQSTAAYTYDILGRRALDALTIPAVGPNRYLTRYSGCDV 120  
 QY 121 VELNPISNVDDMTSAAKEKKGPFESVYWFYIKGDDDEDKYCPTRYREYRCGVOL 180  
 DB 121 VELNPISNVDDMTSAAKEKKGPFESVYWFYIKGDDDEDKYCPTRYREYRCGVOL 180  
 QY 181 LSCCAVSAOMAVNDYVPSYLVSRNGAGLTFTPTALSGOYLTLTKIGRFAOTALVLE 240  
 DB 181 LSCCAVSAOMAVNDYVPSYLVSRNGAGLTFTPTALSGOYLTLTKIGRFAOTALVLE 240  
 QY 241 VNDRCIKIGSQNLFLPSKCMWTEOYOTGFGGHELYPIADNTRHADVYRGYEDILQRMN 300  
 DB 241 VNDRCIKIGSQNLFLPSKCMWTEOYOTGFGGHELYPIADNTRHADVYRGYEDILQRMN 300  
 QY 301 NLRRKNPSAPDRPDSVPOEIPAVYTKKAGRTPDASSSEKKAPPESEDDMOAEASGEN 360  
 DB 301 NLRRKNPSAPDRPDSVPOEIPAVYTKKAGRTPDASSSEKKAPPESEDDMOAEASGEN 360  
 QY 361 PALPEDDEVPEDETHDDPDDPDYNDMPAVIPVEETTKSSNAVSMPITAAFAACVAL 420  
 DB 361 PALPEDDEVPEDETHDDPDDPDYNDMPAVIPVEETTKSSNAVSMPITAAFAACVAL 420  
 QY 421 VGLIWSIVYKARS 434  
 DB 421 VGLIWSIVYKARS 434

RESULT 7

AAP90887 standard; protein; 393 AA.

AC AAP90887;  
 XX  
 AC AAP90887;  
 XX

DT 16-NOV-1989 (first entry)

DE Herpes Simplex virus-1 gD protein.

KW Herpes Simplex virus-1; gD protein; diagnostic test kit.

KW membrane-free polypeptide; antibody; anti-antibody; detection.

OS Herpes simplex virus-1.

PN AU8930061-A.

PD 22-JUN-1989.

PF 17-FEB-1989; 89AU-0030061.

PR 30-AUG-1983; 83AU-0030061.

PA (GERTH ) GENENTECH INC.

PI Herman PW, Lasky LA;

DR WPI; 1989-234099/33.

PT Diagnostic test kit - contains molecularly cloned, truncated  
 CC membrane-free deriv. of polypeptide and complementary antibody  
 CC or anti-antibody.

PS Disclosure; fig 1; 88pp; English.

CC Herpes Simplex virus-1 gD protein (see AAN90524). The DNA was  
 CC used to make truncated membrane-free derivs.  
 CC with antigenic determinants capable of specifically binding  
 CC complementary antibody (Ab). The patent claims  
 CC a diagnostic kit contg. the deriv. and the Ab or anti-Ab,  
 CC for detecting HSV infection. See AAN90523-6, AAN90529-30, AAP90165,  
 CC and AAP90166.

SO Sequence 393 AA:

Query Match 8.5%; Score 197; DB 10; Length 393;  
 Best Local Similarity 24.3%; Pred. No. 2.2e-09;

Matches 78; Conservative 48; Mismatches 145; Indels 50; Gaps 14;

QY 113 RVSRGCDVLELNPISNVDDMTSAAKEKKGPFESVYWFYIKGDDDEDKYCPTRYREY 172  
 DB 85 RVSRGCDVLELNPISNVDDMTSAAKEKKGPFESVYWFYIKGDDDEDKYCPTRYREY 172  
 QY 173 REGGDVOLLSECAVSAOMAVNDYVPSYLVSRNGAGLTFTPTALSGOYLTLTKIGR 231  
 DB 140 TESCYNKSLGACPLRTIPRM--NTYDSFSAVSEDDNLFMHAPFETAGTYLRVAKINDW 197  
 QY 232 AOTALVLE--VNDRCIKIGSQNLFLPSKCMWTEOYOTGFGGHELYPIADNTRHADVY 289  
 DB 198 TETIQFLEHRAKSGC-KYTLPLRIPPSACLSPGAYQGVTVDSIGML---PRFIPEN 252  
 QY 290 RG---YEDIIQRMNNLRRKNPSAPDRPDSVPOEIPAVYTKKAGRTPDASSSEKKAPPE 346  
 DB 253 RTVAVSLKLAGWH-----GPRAP-YTSTLLPELP-----ETPN--TOPELAPE 295  
 QY 347 DSEDD--MQAASGENPALPEDDEVPEDETHDDPDDPDYNDMPAVIPVEETTKSSNAV 405  
 DB 296 DPEDSALLEDPGVTAQOIPPMHPIESIQDAATPIPHPAIPNNMGLI-----AGAV 346  
 QY 406 SMPITAAFAACVALVGLVW 426  
 DB 347 GGSLLAALVIC-----GIYVW 362

RESULT 8

AAR06489 standard; protein; 369 AA.

AC AAR06489;  
 XX  
 AC AAR06489;  
 XX

DT 07-JAN-1991 (first entry)

DE Polypeptide with activity of surface protein gD.

KW

```

OS   HSV-1 Miyama strain.
XX   Surface protein gD.
KM   JP02182196-A.
XX   16-JUL-1990.
XX   15-DEC-1988; 88JP-0317546.
XX   25-MAR-1988; 88JP-0072596.
XX   19-JUL-1988; 88JP-0180114.
XX   15-DEC-1988; 88JP-0317546.
PA   (TAKE ) TAKEDA CHEMICAL IND KK.
XX   WPI; 1990-258264/34.
XX   DR N-PSDB; AAQ05677.
XX   New polypeptide with similar biological activity - to surface
PT   protein gD of HSV-1 Miyama strain produced by genetic technology
XX   Disclosure; Fig 1; 20pp; Japanese.
XX   The polypeptide is expressed from DNA in an E.coli host.
XX   Sequence 369 AA;
SQ
Query Match      8.2%; Score 190; DB 11; Length 369;
Best Local Similarity 23.2%; Pred. No. 9e-09; Indels 66; Gaps 14;
Matches 78; Conservative 47; Mismatches 145;
XX   106 PYRNYLTRVSRGCDVVELNPISNVDMMISAKEKEKGFPEASVWFYVIKGDGEDKYC 165
XX   54 PITVYVAVLERACRSVLNAPSEAPQIVRGASEDVARKQYNLTIAFRM-----GNCAL 108
XX   166 PIKREYRECGDVQLISECAVOSQOMWADVPS-TLVSRNAGLTIFSPALSGOYL 224
XX   109 PITVMEYTEGYSNKSIGACPIRTQPRW--NYDSEFSAVEDNGLFMAHAPAFETAGTYLR 166
XX   225 TLKIGRFAQTALVLE--VNDRCIKIGSQLNLFPSKWTTEOYTG-----FQG 271
XX   167 LKINDWTEITQFILEHRKSGC-KALPLRIRPSACLSPOAYQOGTVDSIGMLPRFIP 225
XX   272 EHLIYPIADNTRHADVDYRGYEDILQRRNNLLRKKNSAPDRPRDPSPOEIPAVTKKAG 331
XX   226 ENQRTVAVYSLKTAG-----WH-----GPKAP-YTSTLLPEL-----S 258
XX   332 RTPDAESSEKKAPDESED--MQAEASGENPALPEDEVEPEDTEHDPSDPIYNDMP 390
XX   259 ETPNA--TQPELAPDEPDESALLEDPVGTAVAPQIIPNMHIPSIDAAATPHHPATPNNMG 316
XX   391 AVIPEETTKSSNAVSMPIFAFVACAVALVGLIWM 426
XX   317 LI-----AGAVGSLALALVLC-----GIYWM 338
XX
RESULT 9
AAW81601
ID   AAW81601 standard; peptide; 369 AA.
XX
XX   AAW81601;
XX   27-JAN-1999 (first entry)
XX   HSV gD1 peptide fragment.
XX   gD1; Vaccinia cytotoxic T cell response; viral infection; rabies;
KM   peptide-fatty acid conjugate; influenza; oncogene; liposome; APC;
KM   human immune deficiency virus; antigen-presenting cell; antibody;
XX   protection.
XX   Herpes simplex virus.
OS

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XX   US837249-A.
XX   17-NOV-1998.
XX   20-OCT-1993; 93US-0139609.
XX   15-APR-1992; 92US-0868946.
XX   19-APR-1985; 85US-0723087.
XX   08-MAY-1987; 87US-0047443.
XX   12-APR-1991; 91US-0685459.
XX   20-OCT-1993; 93US-0139609.
XX   (WIST-) WISTAR INST.
XX   Dietzschold B, Heber-Katz E;
XX   WPI; 1999-023378/02.
XX   Inducing cytotoxic T cell response against virus using peptide-fatty
PT   acid conjugate - formulated in liposomes with an adjuvant,
XX   specifically for protecting against herpes simplex or rabies viruses
XX   Disclosure; Column 17-20; 21pp; English.
XX
XX   This sequence is a fragment of the Herpes Simplex Virus gD1 peptide which
XX   is used in a method of inducing a cytotoxic T cell response against viral
XX   infection in a mammal by administering a peptide-fatty acid conjugate.
XX   Such conjugates are used particularly to vaccinate against HSV, rabies
XX   and also other viruses such as influenza, human immune deficiency virus
XX   and oncogenic viruses. When the liposomes fuse to an antigen-presenting
XX   cell (APC), the conjugate remains bound to the surface of the APC
XX   membrane and is not degraded inside the cell, which generates a T cell
XX   response without any antibody response, avoiding the risk of immune
XX   enhancement (in which antibodies increase viral infectivity). Such
XX   compounds can provide long-lasting protection from only a single
XX   injection.
XX   Sequence 369 AA;
SQ
Query Match      8.2%; Score 190; DB 20; Length 369;
Best Local Similarity 23.2%; Pred. No. 9e-09; Indels 66; Gaps 14;
Matches 78; Conservative 47; Mismatches 145;
XX   106 PYRNYLTRVSRGCDVVELNPISNVDMMISAKEKEKGFPEASVWFYVIKGDGEDKYC 165
XX   54 PITVYVAVLERACRSVLNAPSEAPQIVRGASEDVARKQYNLTIAFRM-----GNCAL 108
XX   166 PIKREYRECGDVQLISECAVOSQOMWADVPS-TLVSRNAGLTIFSPALSGOYL 224
XX   109 PITVMEYTEGYSNKSIGACPIRTQPRW--NYDSEFSAVEDNGLFMAHAPAFETAGTYLR 166
XX   225 TLKIGRFAQTALVLE--VNDRCIKIGSQLNLFPSKWTTEOYTG-----FQG 271
XX   167 LKINDWTEITQFILEHRKSGC-KYALPLRIRPSACLSPOAYQOGTVDSIGMLPRFIP 225
XX   272 EHLIYPIADNTRHADVDYRGYEDILQRRNNLLRKKNSAPDRPRDPSPOEIPAVTKKAG 331
XX   226 ENQRTVAVYSLKTAG-----WH-----GPKAP-YTSTLLPEL-----S 258
XX   332 RTPDAESSEKKAPDESED--MQAEASGENPALPEDEVEPEDTEHDPSDPIYNDMP 390
XX   259 ETPNA--TQPELAPDEPDESALLEDPVGTAVAPQIIPNMHIPSIDAAATPHHPATPNNMG 316
XX   391 AVIPEETTKSSNAVSMPIFAFVACAVALVGLIWM 426
XX   317 LI-----AGAVGSLALALVLC-----GIYWM 338
XX
RESULT 10
AAP40083
ID   AAP40083 standard; Protein; 394 AA.
XX

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AC AAP40083;  
 XX  
 DT 12-FEB-1992 (first entry)  
 XX  
 DE Sequence of Herpes simplex virus type 1 gd glycoprotein.  
 XX  
 KW Antigen; vaccine; immunogen.  
 XX  
 OS Herpes simplex virus type 1.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..25  
 FT Protein /label= signal  
 FT Region 26..394  
 FT /label= transmembrane  
 XX  
 PN EPI101655-A.  
 XX  
 PD 29-FEB-1984.  
 XX  
 PE 19-JUL-1983; 83EP-0401476.  
 XX  
 PR 06-JUL-1983; 83US-0510551.  
 PR 20-JUL-1982; 82US-0400028.  
 PR 25-OCT-1982; 82US-0436368.  
 PR 25-JAN-1984; 84US-0573642.  
 XX  
 PA (MOLE-) MOLECULAR GENETICS.  
 PA (AMCY ) AMERICAN CYANAMID CO.  
 XX  
 PI Watson RJ, Weis JH, Enquist LW;  
 DR WPI; 1984-057658/10.  
 DR N-PSDB; AAN40070.  
 XX  
 PT Antigenic herpes simplex polypeptide prodn. - by culturing  
 PT microorganisms contg. vector including viral DNA fragment  
 XX  
 PS Claim 65; Fig 3; 109pp; English.  
 XX  
 CC The inventors claim: (1) purified DNA sequences coding for the gd  
 CC glycoproteins; (2) recombinant DNA vectors contg. these SQs;  
 CC (3) unicellular organisms contg. these DNA SQs or vectors; and  
 CC (4) polypeptides prepd. by these transformed organisms. The pref'd.  
 CC host organism is E.coli ATCC 39159, 39160, B-15451 or B-15471 (see  
 CC AAN40070/P40083) or B-15449 or B-15450 (see AAN40071/P40084).  
 XX  
 SQ Sequence 394 AA;  
 Query Match 8.2%; Score 190; DB 5; Length 394;  
 Best Local Similarity 23.2%; Pred. No. 9.9e-09;  
 Matches 78; Conservative 47; Mismatches 145; Indels 66; Gaps 14;

QY 391 AVIPVEETTKSSNAVMPFPAFVACAVALVGLV 426  
 DB 342 LI-----AGAVGSGSLAALVLC-----GIYVW 363  
 RESULT 11  
 AAP50582  
 ID AAP50582 standard; Protein; 394 AA.  
 XX  
 AC AAP50582;  
 XX  
 DT 27-NOV-1991 (first entry)  
 XX  
 DE Sequence encoded by herpes simplex virus -1 (HSV-1) glycoprotein  
 DE D (gd) gene.  
 XX  
 KW Glycoprotein; antigen; immunogen; vaccine.  
 XX  
 OS Herpes simplex virus -1.  
 XX  
 PN A08432423-A.  
 XX  
 PD 07-MAR-1985.  
 XX  
 PE 27-AUG-1984; 84AU-0032423.  
 XX  
 PR 09-MAR-1984; 84US-0568170.  
 PR 30-AUG-1983; 83US-0527917.  
 PR 31-OCT-1983; 83US-0547551.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Lasky LA, Berman FW;  
 DR WPI; 1985-099047/17.  
 DR N-PSDB; AAN50489.  
 XX  
 PT - useful for giving protection against herpes simplex virus  
 PT vaccine contg. poly. peptide with exposed antigenic determinants  
 XX  
 PS Example; Fig 1; 93pp; English.  
 XX  
 CC The inventors claim a novel vaccine which contains a membrane-bound  
 CC polypeptide having exposed antigenic determinants capable of raising  
 CC neutralizing antibodies against a pathogen. Alternatively, the  
 CC vaccine contains a truncated membrane-free deriv. The pref.  
 CC polypeptide is esp. a glycoprotein of herpes simplex virus types 1  
 CC or 2, and the virus is the pathogen. The glycoprotein is a gc and/or  
 CC gd. See also A08432424.  
 XX  
 SQ Sequence 394 AA;  
 Query Match 8.2%; Score 189; DB 6; Length 394;  
 Best Local Similarity 23.5%; Pred. No. 1.2e-08;  
 Matches 79; Conservative 46; Mismatches 145; Indels 66; Gaps 14;

QY 332 RPPDESSSEKKAPDEDESD-MQASAGENPALPEDEVEDPTEHDDPNPDYNDMP 390  
 DB 284 ETPMA--TOPELAPDEPDESDLEDPVGTAVPQIPNNHPISTIGDAATPYHPAPPNMG 341  
 QY 391 AVIPVEETKSSNNAVSMPIFAFVACAVALLVW 426  
 DB 342 LI-----AGAVGSLALALVLC---GIYVW 363

RESULT 12  
 ID AAR21777 standard; Protein: 442 AA.  
 AC AAR21777;  
 DT 10-JUN-1992 (first entry)  
 DE EHV-1 envelope glycoprotein D protein.  
 KW Equine Herpes Virus-1; g D; vaccination; respiratory;  
 KW disease; abortion; neurological disorders.  
 OS Equine hepatitis virus.  
 XX  
 XX Key Location/Qualifiers  
 FT Cleavage-site 57..58 /note="cleaves signal peptide"  
 FT Protein 58..442 /label="EHV-1\_gd  
 FT Region 80..93 /note="peptide 1 - antigenic epitope"  
 FT Region 343..361 /note="peptide 2 - antigenic epitope"  
 FT Modified-site 103..105 /note="N-glycosylation site"  
 FT Modified-site 111..113 /note="N-glycosylation site"  
 FT Modified-site 347..349 /note="N-glycosylation site"  
 FT Modified-site 396..398 /note="N-glycosylation site"  
 FT Modified-site 405..422 /note="N-glycosylation site"  
 FT Domain /note="membrane spanning domain"  
 PN MO9202252-A.  
 XX  
 XX 20-FEB-1992.  
 PD 25-JUL-1991; 91WO-US05284.  
 PF 01-AUG-1990; 90US-0561553.  
 PR (RESE ) RES CORP TECHN INC.  
 PA O'Callaghan DJ;  
 PI WPI; 1992-079808/10.  
 DR N-PSDB; AAQ21883.  
 XX  
 XX DNA encoding equine herpes virus-1 envelope glyco:protein -  
 PT useful in preparation of vaccine composition for immunising  
 PT against herpes infection  
 PS  
 PS Claim 9; Fig 2; 65pp; English.

The equine hepatitis virus-1 envelope glycoprotein D (EHV-1 gd) protein was expressed as a fusion protein with beta-galactosidase using a lambda gt11 expression vector. The resultant recombinant molecules were packaged into lambda phage heads and the phage used to transfect E. coli KM 392 cells in the presence of X-gal. The EHV-1 gd polypeptide was batch purified from the lysate using an anti-beta galactosidase antibody linked to a Sepharose 4-B immuno-affinity column. EHV-1 gd purified in this way was of sufficient

CC purity for production of anti-EHV-1 gd antibodies. The polypeptide  
 CC of EHV-1 gd and its fragments are useful in a vaccine compsn. for  
 CC passive immunisation of mammals against EHV-1 and hence the associated  
 CC respiratory disease, abortions or neurological disorders.  
 XX

SO Sequence 442 AA;  
 Query Match 8.0%; Score 184.5; DB 13; Length 442;  
 Best Local Similarity 22.1%; Pred. No. 3.8e-08;  
 Matches 96; Conservative 59; Mismatches 170; Indels 109; Gaps 20;

QY 18 VLNKHMDCGGRCCSGAAVFTLEWTCVIRIMREHICFRNMDHLFRNFWIVLLSR 77  
 DB 70 ILSVYLSG-----TCKAKRA---VRGRDR----- 93  
 QY 78 ASOSTAAVITYDY-ILGRALDALITPAVG-----YNRYLTVRSRGCVYELNPSVDDM 132  
 DB 94 -PREVPPRYNYTILFRYNATLVPFINOVKNVDRLRYTATRPCEMIALAKTNIDSI 152  
 QY 133 ISAKKEKEKGPPEASVWYVYKGDDEKTC--FIYKREYECGDVOLLSECAVQSAQ 190  
 DB 153 LKELAAAKTYP--ARLTWEKIM-----PTCATPIHDVSYMKCKPKLSFAMCDERSDI 203  
 QY 191 MMAVDYVPSYLVSNGAGLITFPTAALSGOYLTLTKI-GRFAQTALVTLVENDRCLTKG 249  
 DB 204 LMQASLITMAETDDELGLVLAAPASASGLVRRVETIGRRITYDFSVTISERC-PIA 262  
 QY 250 SOLNF-LPSKCVTEQYQYG-----FOGEHLPIADITRRHAD-----DYRGYEDILQ 297  
 DB 263 FELNFGNPDRCKTPEQYSRGEVTRFRFLCEFNPGQ-----HMTWVKFWFYVDGGLPQ 318  
 QY 298 RWNMLRKKNPSPADPRP--DSVPOELPAVTAKBERTDASSSEKKAPDESEDDMQAE 355  
 DB 319 FYEGQAFAR-PVPPDHPGFDVSEET-----TONKTDPKKGQADPPRN 361  
 QY 356 ASGENPA---ALPEDEVEDTEHDDPNPDYNDMPAVIPEETKSSNNAVSMPIFAA 412  
 DB 362 OFPKMPSIKHLVRLDEVEDEVIE-----PATRKPK--TSSNSTFVGISVG 405  
 QY 413 FVACAVALLVW 426  
 DB 406 LGIAGLVGVILY 419

RESULT 13  
 AAM11323  
 ID AAM11323 standard; Protein: 388 AA.  
 AC AAM11323;  
 DT 29-APR-1997 (first entry)  
 DE HSV glycoprotein D variant gd-1(del290-299).  
 KW HSV; glycoprotein D variant; gd-1(del290-299); antiviral;  
 KW virucide.  
 XX  
 XX Herpes simplex virus type 1 strain Patton.  
 XX  
 XX Key Location/Qualifiers  
 FT Peptide 1..25 /label="Sig-peptide  
 FT Protein 26..388 /label="Mat protein  
 FT /note="The mature protein has amino acids 290-299  
 of the wild-type gd-1 replaced by  
 Arg-Lys-Ile-Phe"  
 PN W09703199-A1.  
 XX 30-JAN-1997.  
 PD 03-JUL-1996; 96WO-US11344.

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XX 07-JUL-1995;          95US-0499568.
PR
XX (COMP-) COMPETITIVE TECHNOLOGIES INC.
PA
XX Cohen GH, Eisenberg RJ, Nicola A;
PI
XX MPI; 1997-119054/11.
DR
XX N-PSDB: AAT51318.
XX Variant Herpes Simplex virus glycoprotein D molecule - contains
PT mutation in region IV of the glycoprotein, used for inhibiting
PT infection of susceptible cells by HSV
XX
PS Example 1; Page 30-31; 57pp; English.
XX
CC A variant herpes simplex virus (HSV) glycoprotein D (AAW11322),
CC designated gp-1(del290-299) has amino acid residues 290-299 (in
CC region IV) of HSV-1 Patton strain gp-1 replaced by Arg-Lys-Ile-Phe.
CC A DNA sequence encoding the variant gp-1 is given in AAT51317. Region
CC IV of gp-1 is required for entry of HSV into susceptible cells.
CC The gp-1 variant has antiviral activity and can be used to prevent
CC or ameliorate HSV infection. Another variant, gp-1(del290-299t),
CC which has patric. potent antiviral activity, has an additional
CC mutation in the transmembrane region of gp-1.
CC
SO Sequence      388 AA;
Query Match           7.7%, Score 179; DB 18; Length 388;
Best Local Similarity 23.4%; Pred. No. 1e-07;
Matches 79; Conservative 41; Mismatches 142; Indels 76; Gaps 13;
QY 106 PYNRLTRVSRGCDVVELNPISNVDDMSAAKEKGGPFEEASVVFYIKRQDGEDKYC 165
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 79 PITVVYAVLERACRSVLLNAPSEADQIVRGASEDVKKOPYNTLTAMFRY----GCNCAl 133
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 166 PYRKREYREGCGVOLLSCEAVOSAGMWADVPS--TLVSNGAGLTSPFAALSGOYL 224
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 134 PITWEIYECSGNKSLGACPIRTQRR--NYTDSFSAVSEDNLGLMAHPAFETAGTYLR 191
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 225 TLKIGRFQAOTALVTLE--VNDRCLTKIGSOLNFLPKSCWTTEQYQGFQGEHLYPYADNT 282
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 192 LVKINDWFETIQFILEHRAKGSC-KYALPLRLRPFSACLSPQAYQGQGVYVDSIGML----- 245
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 283 RHADDVYNGIEDILQRNNLKRKKRPSADPPSDSVPOEIPAVT---KKAEGRPDDES 338
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 246 -----PREIFPENQRTVAAYSUKIAQWHGPKAPY 273
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 339 SEKKARPEDSE--DDMQAEASGENP--AALPED--DEVPEDTEHDND--PRSDDYND 388
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 274 TSTLLPELPSETPNKTQPELAPEDEDNSLEDVGYVAPOCKITODAAATPHHPATPTN 333
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 389 MPAAVIPVEETTKSSNAVSMPIFAAFVACAVALVGLLV 426
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 334 MGLI-----AGAVGGSLAALVIC-----GIYVW 357
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 14
ID AAR11273
XX AAR11273 standard; Protein: 435 AA.
XX
XX AAR11273;
XX
XX 30-MAY-1991 (first entry)
XX
DE HSV-1 antigen/heat-labile enterotoxin B subunit fusion protein.
XX
XX Fusion protein; Herpes Simplex Virus-1; HSV-1; heat-labile enterotoxin;
KW subunit B; LTB; vaccine; nasal mucosa tissue; gd.
XX
XX HSV-1 strain Miyama, Homo sapiens.
XX
XX EP418626-A.

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	XX	PD	27-MAR-1991.	
	XX	PB		
	XX	PF	03-SEP-1990; 90EP-0116878.	
	XX	PR	08-SEP-1989; 89JP-0233728.	
	PA	(TAKE ) TAKEDA CHEMICAL IND KK.		
	PI	Fujisawa Y, Hinuma S, Mayumi A, Yamamoto T;		
	DR	WPJ: 1991-088294/13.		
	PP	P-PStDB; R112732.		
	PT	Fused protein used to treat viral and pathogenic bacterial		
	PS	Infections - cong. heat labile enterotoxin B sub-unit and eg		
	SS	herpes-simplex virus antigen		
	TS	Disclosure; Fig 12; 34pp; English.		
	CC	A desired truncated gene is cut out from a plasmid in which the		
	CC	truncated gD gene of HSV-1 strain Miyama was chemically synthesised.		
	CC	An appropriated linker is added to it as needed, followed by		
	CC	a construction of a fused gene in which an Ltnb gene is linked to the		
	CC	3' end. The resulting fused protein gene is ligated downstream from		
	CC	a promoter in an expression vector.		
	CC	The product is effcient for targeting to nasal mucosa tissues		
	CC	compared to unfused proteins. It can induce an immune response.		
	CC	The protein is useful as immunogen in vaccines for therapeutic and		
	CC	preventive use, or for treatment of viral, pathogenic protozoan or		
	CC	bacterial infections.		
	SQ	See also AAQ11073.		
	Sequence	435 AA:		
	Query Match	7.3%; Score 169; DB 12; Length 435;		
	Best Local Similarity	23.8%; Pred. No. 9.9e-07;		
	Matches	72; Conservative 37; Mismatches 123; Indels 70; Gaps 13;		
OY		96 LDALTIP-----VG-----PYNRYLTRVSRGCDVVELNPNISNVDDMSIAA 136		
Dd		50 LDPLDPAGVRVHYHQGLPDPFPSPSLPVVVYAVERACRSVLNAPSEAPDIVNGCA 109		
OY		137 KEKKGGEFEASVMVEFYIKGDGEDDKCPTRYKRRECGDVQLLSECVAOSQAOMAYDY 196		
Dd		110 SEDVKRKYNYNLTIAFRM----GGNCALPIITVMEYTECSYNSLGACPINFQPWM--NY 162		
OY		197 VPS-TVLEIRNGAGLTIFSPITALSGOYLTLTKIGRAOTATYLE--VNDRCLKTGSOLN 253		
Dd		163 YDSFSAVEDNLGIFLMAHAPAEFTACTGYLRKVKNINWTELTQTPLLHRAKGSC-KIALPLR 221		
OY		254 FLPSCKWTETEOYTQS-----FOGHLYPIADTNTRHADVDYGREDIILGRMNLL 302		
Dd		222 IPPSACLSPQAVQQGVTVDSICMLPRFIPENRGTVAAYVSLSLAG-----WH-- 267		
OY		303 LRKKRPASPDRPDSVPDEIRAIVTYTKKAGCRIPDAASSEKKARPESSEDMDQEAEGENPA 362		
Dd		268 ----GPKPAP-TYSTILLPEEL-----SETPNNA--TOPELAPEDEDLSAPTSSSTRKT 312		
OY		363 AL 364		
Dd		313 QL 314		
	RESULT 15			
	AAWI1322			
ID	AAWI1322 standard; Protein; 308 AA.			
XX	AAWI1322;			
AC				
DT	29-APR-1997 (first entry)			
XE	HSV glycoprotein D variant gd-I(delta)290..299(c).			

[illegible]

```

Db      223 -----PREIFENQRTVAVYSLKTAGHGRAPY 250
QY      339 SEKKAPEDSEDDMQAEASGENPALPEDDEVPDTE-HDDP 379
          :   ||| ||      :   ||| ||| :   ||
Db      251 TSTLLPELSE-----TPNMTQPLAED---PEDSLALDDP 284

```

Search completed: February 19, 2003, 16:23:31  
Job time : 84 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 19, 2003, 16:21:10 ; Search time 21 Seconds

(without alignments)  
1986.778 Million cell updates/sec

Title: US-09-994-064-11

Sequence: 1 MRPPLRRHSRYAKGEVLN.....ACAVLVGLWSTVCANS 434

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 segs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

Database : PIR 73: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	190.5	8.2	393	1 VGBEDZ	glycoprotein D pre
2	190	8.2	394	1 VGBED1	glycoprotein D - h
3	190	8.2	394	1 VGBED17	glycoprotein D pre
4	187	8.1	394	1 A47627	glycoprotein D pre
5	181	7.8	442	1 VGBEEA	glycoprotein D pre
6	175	7.6	452	1 VGBEG3	glycoprotein D pre
7	165	7.1	402	1 VGBE50	glycoprotein D pre
8	158	6.8	393	1 VGBE33	glycoprotein D pre
9	158	6.8	393	2 E43674	glycoprotein D pre
10	156.5	6.8	393	1 VGBED2	glycoprotein D - h
11	148.5	6.4	380	2 H48552	glycoprotein D - h
12	146	6.3	402	2 JQ2164	glycoprotein D pre
13	146	6.3	402	2 T42615	glycoprotein D pre
14	144	6.2	417	1 VGBE1B	glycoprotein D pre
15	139.5	6.0	417	2 S35784	glycoprotein D pre
16	131.5	5.7	384	2 JQ2351	glycoprotein D pre
17	129	5.6	498	1 VGBEGX	glycoprotein D pre
18	116	5.0	976	2 S40697	secreted glycoprot
19	113.5	4.9	307	2 TQ4141	processing endopro
20	108.5	4.7	395	1 JQ1746	histone deacetylase
21	106.5	4.6	509	2 T34871	glycoprotein D pre
22	106.5	4.6	501	2 A49227	probable membrane
23	106	4.6	727	2 B40439	sialidase - Actino
24	106	4.6	764	2 A40439	UBF transcription
25	105.5	4.6	2499	1 A30788	mannose 6-phosphat
26	105	4.5	574	2 S37762	225K protein - Bab
27	104.5	4.5	1643	2 T14274	versican precursor
28	104.5	4.5	2911	2 T20566	hypothetical prote
29	104.5	4.5	3381	2 T42389	versican precursor

30	104	4.5	539	2 T15871	hypothetical prote
31	103	4.5	300	2 JQ2220	hydroxypoline-ric
32	103	4.5	708	2 D96711	hypothetical prote
33	103	4.5	727	2 S18193	autoantigen NOR-90
34	103	4.5	764	2 S09318	transcription fact
35	103	4.5	1881	2 H95076	zinc metalloprotei
36	103	4.5	7962	2 I38346	elastic titin - hu
37	103	4.5	26926	1 I38344	titin, cardiac mus
38	102.5	4.4	416	1 SKX14G	dermal gland prote
39	102.5	4.4	856	2 T16543	hypothetical prote
40	101	4.4	651	2 S18874	nucleolin - Africa
41	101	4.4	727	2 JC5113	ribosomal transcr
42	101	4.4	764	2 JC5112	ribosomal transcr
43	101	4.4	855	2 D98004	histidine Nuclei-Co
44	101	4.4	1211	2 T42230	Af4 protein - mous
45	101	4.4	1277	2 T14152	synaptic scaffold1

## ALIGNMENTS

RESULT 1					
VGBEDZ					
glycoprotein D precursor - human herpesvirus 1 (strain Hzt)					
C:Species: human herpesvirus 1					
C>Date: 31-Dec-1993 #sequence-revision 31-Dec-1993 #text-change 09-Sep-1994					
C:Accession: A90945; A03729					
R:Lasky, L.A.; Dowbenko, D.J.					
DNA 3, 23-29, 1984					
A:Title: DNA sequence analysis of the type-common glycoprotein-D genes of herpes s.lm.					
A:Reference number: A90945; MUID:8411545; PMID:6321120					
A:Accession: A90945					
A:Molecule type: DNA					
A:Residues: 1-393 <LAS>					
A:Cross-references: GB:K02372					
C:Superfamily: herpesvirus glycoprotein D					
C:Keywords: glycoprotein; transmembrane protein					
F:1-20/Domain: signal sequence #status predicted <Sig>					
F:21-393/Product: glycoprotein D #status predicted <GPD>					
F:341-360/Domain: transmembrane #status predicted <TM>					
F:118,145,286/Binding site: carbohydrate (Asn) (covalent) #status predicted					
Query Match					
Best Local Similarity 8.28; Score 190.5; DB 1; Length 393;					
Matches 80; Conservative 49; Mismatches 139; Indels 75; Gaps 15;					
QY	99	LTIPAVGPYRNYLTVRSRGCDVVELNPISNVDMISAKEKGPPEASVYVYIKGD	158		
DB	80	ITVYAV-----LEBACRSVLLNAPSEAPQIVRGASEDVRRKQYNLTIAFRM----	126		
QY	159	DGEDKCPPIYRKERYREGDVOQLSECAVQSAQMAVDVYS-TLVSRNAGLTFSPAA	217		
DB	127	-GGCAIPITVMEYTECSYNSLIGACPIRQPRW--NYVSFSVSDNIGFLMHAFAFE	183		
QY	218	LSGGYLLTKIGRFAQATATLE--VNDRCIKISQNLPLPSKQWTEYOYTG-----	268		
DB	184	TAGYLLVKNIDMTETTOGLEHRAKGC-KYALPLRIPPSALSQAATQOGTVDSIG	242		
QY	269	---FOGHNLYPIADITRHNADVRYGVEDITLQNMNLLRKNPSADPPRDSVQEPFA	324		
DB	243	MLRPFIEHQRTVAVYSLKTIAG-----WH-----GPRAP-YVSTLLRPLP-	282		
QY	325	VTKAAGRTPDAAESSEKKAPPESEDD-MQAEASGENPALPEDDEVPEDETHDPPSDP	383		
DB	283	-----ETPNA--TQELAPBEDPESALLEDPRGTVAPOIPRMWHIPSIDQATPRNRP	333		
QY	384	DYVNDMPAVYIVPEETTKSSNNAVSPFAAFVACAVLVGLVW	426		
DB	334	ATPRNMGLT-----AGAVGSLAALVYC-----GIYVW	362		
RESULT 2					
VGBED1					

glycoprotein D - human herpesvirus 1

C:Species: human herpesvirus 1

C>Date: 05-Apr-1983 #sequence\_revision 05-Apr-1983 #text\_change 16-Jul-1999

C:Accession: A94268; B90945; A03729

R:Matson, R.J.; Weis, J.H.; Salstrom, J.S.; Engquist, L.W.

Science 218, 381-384, 1982

A>Title: Herpes simplex virus type-1 glycoprotein D gene: nucleotide sequence and expres

A:Reference number: A94268; MUID:83016630; PMID:6289440

A:Accession: A94268

A:Molecule type: DNA

A:Residues: 1-394 <WAT>

A:Cross-references: GB:J02217; NID:9330100; PIDN:AAA45785.1; PID:9330101

A:Experimental source: strain Patton

A>Note: a strongly hydrophobic region of 25 amino acids between residues 340 and 364 is

RNA 3, 23-29, 1984

A>Title: DNA sequence analysis of the type-common glycoprotein-D genes of herpes simplex

A:Reference number: A90945; MUID:84131549; PMID:6321120

A:Accession: B90945

A:Molecule type: DNA

A:Residues: 1-3, 'A', 5-70, 'N', 72-83, 85-269, 'R', 271-282, 'P', 284-364, 'R', 366-394 <LAS>

A:Experimental source: strain Hst

C:Superfamily: herpesvirus glycoprotein D

C:Keywords: glycoprotein; transmembrane protein

F:119,146,287/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 8.2%; Score 190; DB 1; Length 394;

Best Local Similarity 23.2%; Pred. No. 4.5e-07;

Matches 78; Conservative 47; Mismatches 145; Indels 66; Gaps 14;

QY 106 PYNRYLTRVSRGCDVVELNPISNDVMSAKKEKGFPEASVWFYIKGDGDEKVC 165

DB 79 PITVYVAVLERACRSVILNAPSEAPQIVRGASEDVRRQPNLTIAFRM-----GGNCAI 133

QY 166 PIYKREYRECGDVOLLSECAVQSAQMAVDPVS-TLVSRNGAGLTIFSPALSGOYL 224

DB 134 PITVMEYTECSYKSLGACPIRTQPRW--NYDSFSAVSNDNGFLMHAFAETACTYLR 191

QY 225 TLKIGRFAQALVTLF--VNDRCIKIGSQLNPLPSKWTTEOYGTG-----FQG 271

DB 192 LVKINDWTEITQFLEHRAKGC-KYALPLRIIPSAQLSPQAVQOQVTVDSIGMLPRFIP 250

QY 272 EHLPIADNTNRHADVYRGYEDILQRMNNILRKKNSAPDRPDSVPOEIPAVTKKAG 331

DB 251 ENORTVAVVSLKTAG-----WH-----GPKAP-YSTILLPEL-----S 283

QY 332 RTDPAESSEKKAPPEDESD-MQEAASGENPALPEDEDEPETHDDPNSDPDYNDMP 390

DB 284 ETPNA--TQELAPDEDESDALIEDVGVAPQIPPNMHIPSTIODAATFYHPPATPNMG 341

QY 391 AVLPVEETKSSNAVSMPIFAFVACAVLVGLLW 426

DB 342 LI-----AGAVGSLIALALVIC-----GIVW 363

### RESULT 3

VCBE17

glycoprotein D precursor - human herpesvirus 1 (strain 17)

C:Species: human herpesvirus 1

A:Date: host Homo sapiens (man)

C:Date: 17-Mar-1987 #sequence\_revision 17-Mar-1987 #text\_change 16-Jun-2000

C:Accession: A03730

R:McGeoch, D.J.; Dolan, A.; Donald, S.; Rixon, F.J.

J. Mol. Biol. 181, 1-13, 1985

A>Title: Sequence determination and genetic content of the short unique region in the ge

A:Reference number: A00656; MUID:85160822; PMID:2984429

A:Accession: A03730

A:Molecule type: DNA

A:Residues: 1-394 <MCG>

A:Cross-references: GB:X14112; NID:91944536; PIDN:CAA32283.1; PID:959564

C:Superfamily: herpesvirus glycoprotein D

C:Keywords: glycoprotein; transmembrane protein

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-394/Product: glycoprotein D #status predicted <GPD>

F:342-358/Domain: transmembrane #status predicted <TMN>

F:119,146,287/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 8.2%; Score 190; DB 1; Length 394;

Best Local Similarity 23.2%; Pred. No. 4.5e-07;

Matches 78; Conservative 47; Mismatches 145; Indels 66; Gaps 14;

QY 106 PYNRYLTRVSRGCDVVELNPISNDVMSAKKEKGFPEASVWFYIKGDGDEKVC 165

DB 79 PITVYVAVLERACRSVILNAPSEAPQIVRGASEDVRRQPNLTIAFRM-----GGNCAI 133

QY 166 PIYKREYRECGDVOLLSECAVQSAQMAVDPVS-TLVSRNGAGLTIFSPALSGOYL 224

DB 134 PITVMEYTECSYKSLGACPIRTQPRW--NYDSFSAVSNDNGFLMHAFAETACTYLR 191

QY 225 TLKIGRFAQALVTLF--VNDRCIKIGSQLNPLPSKWTTEOYGTG-----FQG 271

DB 192 LVKINDWTEITQFLEHRAKGC-KYALPLRIIPSAQLSPQAVQOQVTVDSIGMLPRFIP 250

QY 272 EHLPIADNTNRHADVYRGYEDILQRMNNILRKKNSAPDRPDSVPOEIPAVTKKAG 331

DB 251 ENORTVAVVSLKTAG-----WH-----GPKAP-YSTILLPEL-----S 283

QY 332 RTDPAESSEKKAPPEDESD-MQEAASGENPALPEDEDEPETHDDPNSDPDYNDMP 390

DB 284 ETPNA--TQELAPDEDESDALIEDVGVAPQIPPNMHIPSTIODAATFYHPPATPNMG 341

QY 391 AVLPVEETKSSNAVSMPIFAFVACAVLVGLLW 426

DB 342 LI-----AGAVGSLIALALVIC-----GIVW 363

RESULT 4

glycoprotein D precursor - human herpesvirus 1 (strain ANG)

C:Species: human herpesvirus 1

C:Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 16-Jul-1999

C:Accession: A47627

R:Izumi, K.M.; Stevens, J.G.

J. Exp. Med. 172, 487-496, 1990

A>Title: Molecular and biological characterization of a herpes simplex virus type 1 (

A:Reference number: A47627; MUID:90324869; PMID:2165127

A:Accession: A47627

A:Molecule type: DNA

A:Residues: 1-394 <IDU>

A:Cross-references: GB:X54361; NID:960414; PIDN:CAA38245.1; PID:960415

C:Superfamily: herpesvirus glycoprotein D

C:Keywords: glycoprotein; transmembrane protein

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-394/Product: glycoprotein D #status predicted <GPD>

F:342-360/Domain: transmembrane #status predicted <TMN>

F:119,146,287/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 8.1%; Score 187; DB 1; Length 394;

Best Local Similarity 23.5%; Pred. No. 7.6e-07;

Matches 77; Conservative 46; Mismatches 155; Indels 50; Gaps 14;

QY 106 PYNRYLTRVSRGCDVVELNPISNDVMSAKKEKGFPEASVWFYIKGDGDEKVC 165

DB 79 PITVYVAVLERACRSVILNAPSEAPQIVRGASEDVRRQPNLTIAFRM-----GGNCAI 133

QY 166 PIYKREYRECGDVOLLSECAVQSAQMAVDPVS-TLVSRNGAGLTIFSPALSGOYL 224

DB 134 PITVMEYTECSYKSLGACPIRTQPRW--NYDSFSAVSNDNGFLMHAFAETACTYLR 191

QY 225 TLKIGRFAQALVTLF--VNDRCIKIGSQLNPLPSKWTTEOYGTGFGGEH---LYPIAD 279

DB 192 LVKINDWTEITQFLEHRAKGC-KYALPLRIIPSAQLSPQAVQOQVTVDSIGMLPRFIP 250

QY 280 TNRHADVYRGYEDILQRMNNILRKKNSAPDRPDSVPOEIPAVTKKAGSRTPDAESS 339

DB 251 ENOR-----IVAVVSLKTAGWH-----GPKAP-YSTILLPEL-----SETPNA--T 289



QY 340 EKKAPPESEDD-MQAEASGENPALPBDDEVEDTEHDDPNSDDPYNDMPAVIPVEET 398  
 Db 290 QPELAPPEDEPSALLEDVGVAPQIPNNMHIPSTQDAATPHPATPNMGLI----- 343  
 QY 339 TKSSNAVSMPIFAAFVACAVALLGLVW 426  
 Db 344 ---AGAVGSLLAALVLC-----GLVW 363

# RESULT 5

glycoprotein D precursor - equine herpesvirus 1 (strain Kentucky A)

C:Species: equine herpesvirus 1  
 C:Date: 31-Mar-1992 #sequence=1 revision 31-Mar-1992 #text\_change 16-Jul-1999  
 C:Accession: A38518  
 R:Flowers, C.C.; Eastman, E.M.; O'Callaghan, D.J.  
 Virology 180, 175-184, 1991  
 A:Title: Sequence analysis of a glycoprotein D gene homolog within the unique short segment  
 A:Reference number: A38518; MUID:91082407; PMID:1845821  
 A:Accession: A38518  
 A:Molecule type: DNA  
 A:Residues: 1-442 <FLO>

A:Cross-references: EMBL:M62923; NID:g330892; PIDN:AAA46081.1; PID:g330893  
 C:Superfamily: herpesvirus glycoprotein D  
 C:Keywords: glycoprotein; transmembrane protein  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-442/Product: glycoprotein D #status predicted <MAT>  
 F:404-422/Domain: transmembrane #status predicted <TM2>  
 F:103,111,347,396/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 7.8%; Score 181; DB 1; Length 442;  
 Best Local Similarity 23.0%; Pred. No. 2,66-06;

Matches 84; Conservative 56; Mismatches 153; Indels 72; Gaps 17;

QY 87 YDY-ILGRALDALITPAVG---YNNYLTRVSGCDVVELNPISNVDMISAAREK 141  
 Db 102 YNYTLITRYNATLALSPINDQVKNVDLRIYATRPCEMIALIKTNIDSLIKELAAOK 161  
 QY 142 GGPPEASVWFYVYIKGDDGEKTC--PYRKEYRECGVOLLSSECAVSAQMAVADYPS 199  
 Db 162 --TYSARLTWFKIM-----PTCATPIHDVSYMKCNPKLSFAMCDESDILMQASLITM 212  
 QY 200 TLVRNAGLITFSPALSGOYLITLTKI--GRFQNALVTELVNDRCLKISQINF--LPS 257  
 Db 213 AAEIDDELGLVLAAPAHASGLYRVEIDGRRIYTDPSVTPSERC--PIAFELFGNPD 271  
 QY 258 KCMTEQYQYG-----FOGELHYPIADTNRHAD---DVRGYEDILQRMNLLRKK 306  
 Db 272 RCKTPEQYSGEVFTRRRLGEFNPQGE---HMTWKFVYVDS--GLLPQVFEAQAFA 326  
 QY 307 NPSAPDPRP--DSVPQELPAVTKAEGRTPAESSEKKAPPESEDDMQAEASGENPA-- 362  
 Db 327 RPVPDDNHPGDVSESEL-----TQNTDKPCQADPKPQDPFKMPSIK 370  
 QY 363 -ALPEDEVPEDTEHDDPNSDDPYNDMPAVIPVEETTKSSNAVSMPIFAAFVACAVALL 421  
 Db 371 HLVRLEDEVLEIE-----PYTKPKK--TSKSNSTFVIGSLVGLIAGLV 414  
 QY 422 GLVW 426  
 Db 415 GVILY 419

# RESULT 6

glycoprotein D precursor - equine herpesvirus 1

C:Species: equine herpesvirus 1  
 A:Note: host Equus caballus (domestic horse)  
 C:Date: 30-Sep-1992 #sequence=1 revision 30-Sep-1992 #text\_change 16-Jul-1999  
 C:Accession: I36802; B36646; PQ0146  
 R:Telord, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.  
 submitted to Genbank, March 1992

A:Description: The DNA sequence of equine herpesvirus-1.

A:Reference number: A36805

A:Accession: I36802

A:Molecule type: DNA

A:Residues: 1-452 <TEL>

A:Cross-references: GB:M6664; NID:g330791; PIDN:AA02507.1; PID:g330863

A:Experimental source: strain Ab4P

R:Telord, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.

Virology 189, 304-316, 1992

A:Title: The DNA sequence of equine herpesvirus-1.

A:Reference number: A41831; MUID:92295566; PMID:1318606

A:Contents: annotation; possible protein-coding frames

A:Note: neither amino acid nor nucleotide sequence is given

R:Audonnet, J.C.; Winslow, J.; Allen, G.; Paoletti, E.

J. Gen. Virol. 71, 2969-2978, 1990

A:Title: Equine herpesvirus type 1 unique short fragment encodes glycoproteins with

A:Reference number: A36646; MUID:91108393; PMID:2177089

A:Accession: B36646

A:Molecule type: DNA

A:Residues: 1-452 <AUD>

A:Cross-references: GB:M6664; NID:g330791; PIDN:AA02507.1; PID:g330863

A:Experimental source: strain Kentucky D

R:Elton, D.M.; Halliburton, I.W.; Killington, R.A.; Meredith, D.M.; Bonass, W.A.

Gene 101, 203-208, 1991

A:Title: Sequence analysis of the 4.7-kb BamHI-EcoRI fragment of the equine herpesv1

A:Reference number: JQ0998; MUID:91276272; PMID:1647359

A:Accession: PQ0146

A:Molecule type: DNA

A:Residues: 292-452 <ELT>

A:Cross-references: GB:M6293; NID:g330787; PIDN:AAA66546.1; PID:g808672

C:Genetics:

A:Gene: 72

C:Superfamily: herpesvirus glycoprotein D

C:Keywords: glycoprotein; transmembrane protein

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-452/Product: glycoprotein D #status predicted <MAT>

F:399-419/Domain: hydrophobic <HYD>

F:404-422/Domain: transmembrane #status predicted <TM2>

F:103,111,347,396/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:347,396/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 7.6%; Score 175; DB 1; Length 452;  
 Best Local Similarity 22.6%; Pred. No. 7,96-06;

Matches 84; Conservative 53; Mismatches 149; Indels 86; Gaps 17;

QY 87 YDY-ILGRALDALITPAVG---YNNYLTRVSGCDVVELNPISNVDMISAAREK 141  
 Db 102 YNYTLITRYNATLALSPINDQVKNVDLRIYATRPCEMIALIKTNIDSLIKELAAOK 161  
 QY 142 GGPPEASVWFYVYIKGDDGEKTC--PYRKEYRECGVOLLSSECAVSAQMAVADYPS 199  
 Db 162 --TYSARLTWFKIM-----PTCATPIHDVSYMKCNPKLSFAMCDESDILMQASLITM 212  
 QY 200 TLVRNAGLITFSPALSGOYLITLTKI--GRFQNALVTELVNDRCLKISQINF--LPS 257  
 Db 213 AAEIDDELGLVLAAPAHASGLYRVEIDGRRIYTDPSVTPSERC--PIAFELFGNPD 271  
 QY 258 KCMTEQYQYG-----FOGELHYPIADTNRHAD---DVRGYEDILQRMNLLRKK 305  
 Db 272 RCKTPEQYSGEVFTRRRLGEFNPQGEHMT--MLKFWFYVDS--GLLPQVFEAQAFA 319  
 QY 306 -----KNPSAPDPRP--DSVPQELPAVTKAEGRTPAESSEKKAPPESEDDMQAEAS 357  
 Db 320 YEAQAFARPPDNNHGDVSESEL-----TQNTDKPCQADPKPQDPFKMPSIK 363  
 QY 358 GENPA--ALPEDEVPEDTEHDDPNSDDPYNDMPAVIPVEETTKSSNAVSMPIFAAFV 414  
 Db 364 FKWPSIKHLAPRLDEVLEIE-----PYTKPKK--TSKSNSTFVIGSLVGLG 407  
 QY 415 ACAVALVGLVW 426  
 Db 408 IAGLVGLVILY 419

```

RESULT 7
VGBE50
glycoprotein D precursor - suid herpesvirus 1 (strain Rice)
C:Species: suid herpesvirus 1
A:Note: host Sus scrofa domestica (domestic pig)
C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 16-Jul-1999
C:Accession: A27788
J:Petkovskis, E.A.; Timmins, J.G.; Armentrout, M.A.; Marcholi, C.C.; Yancey Jr., R.J.;
R. Virol. 59, 216-223, 1986
A:Title: DNA sequence of the gene for pseudorabies virus gp50, a glycoprotein without N-
F:18-402/Product: glycoprotein D #status predicted <GPD>
F:362-378/Domain: transmembrane #status predicted <TMN>
A:Accession: A27788
A:Molecule type: DNA
A:Residues: 1-402 <PET>
A:Cross-References: GB:M4001; NID:9334051; PIDN:AAC35203.1; PID:9334052
C:Superfamily: herpesvirus glycoprotein D
C:Keywords: glycoprotein; transmembrane protein
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-402/Product: glycoprotein D #status predicted <GPD>
F:362-378/Domain: transmembrane #status predicted <TMN>

Query Match 7.1%; Score 165; DB 1; Length 402;
Best Local Similarity 21.0%; Pred. No. 4e-05;
Matches 88; Conservative 55; Mismatches 159; Indels 118; Gaps 19;

OY 73 ILSSFASOSTAATVTDYILG-----RRALDALTPAVGPNRYLFR-VSRG 117
Db 6 LLAALVARTTGADVADVAPAPFPFPAYPTYESMQLTLTPSPFVGADVYHTRPLEDP 65
OY 118 CDVVELANPISNVDNISAKEREKGPFEASVWFYVYKGGDEKCP--TYKEYREC 175
Db 66 CGVALLISDPQVDRLNAAVAHRR-PTYRAHVAWYRIADG-----CAHLTYFIEYADC 117
OY 176 GDVQLLSCAVQSAQM---AVDYVPTLVSRNGAGLTIFSPALSGOY--LTETIGR 230
Db 118 DPROVFGRCRRRTTPMWTTPSADYMFPT---EDLGLILMAVGFNFNGQVRLVSVGVN 174
OY 231 FAQTALVTLFVNDRC--LKIGSQLNPLPSKWTTEYOYQTFQGHLYPIADYTRHADY 288
Db 175 ILTFVVALPREGCECPARVDQHTYKFGACMSDSTFKGV-----DV 217
OY 289 YR-----GYEDILQRMNNLLRKNN-----PSAPPRPDSVP 319
Db 218 MRFLTPPYQOPPHREVNYW---YRKNGRITLPRHAHAATPYAIDARPSAGSPRRPRP 273
OY 320 QETPAVTKKAEGRTPDAESSEKKAPED--SEDMQAEASENPAALPEDEVEDTEHDD 378
Db 274 RPRRRPKEPAPATP-----APPDRLEPATRDAAGRPTRPPRPETPH-----R 320
OY 379 PNSDPDYNDMPAVI-----PVEETKSSNAVS---MFFAFAVCAVALVGLVW 426
Db 321 PFAP-----PAVPSGMPQPAEPFOPRTPAAPGVSRHSRYVIGTGMGLLVGVY 373

RESULT 8
VGBE33
glycoprotein D precursor - human herpesvirus 2 (strain 333)
C:Species: human herpesvirus 2
A:Note: host Homo sapiens (man)
C:Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999
C:Accession: A03732
R:Watson, R.J.
Gene 26, 307-312, 1983
A:Title: DNA sequence of the herpes simplex virus type 2 glycoprotein D gene.
A:Reference number: A03732; MUID:84159516; PMID:6323270
A:Accession: A03732
A:Molecule type: DNA
A:Residues: 1-393 <WAT>
A:Cross-References: GB:K01408; NID:9330268; PIDN:AAA5841.1; PID:9330269
C:Superfamily: herpesvirus glycoprotein D
C:Keywords: glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>

```

```

F:25-393/Product: glycoprotein D #status predicted <GPD>
F:340-356/Domain: transmembrane #status predicted <TMN>
F:119,146,287/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 6.8%; Score 158; DB 1; Length 393;
Best Local Similarity 19.9%; Pred. No. 0.00014;
Matches 69; Conservative 55; Mismatches 152; Indels 70; Gaps 12;

OY 97 DALTPAVGPNRYLTRSRGCDVVELNPISNVDNISAKEREKGPFEASVWFYVYK 156
Db 71 DFPQPSI-PTTYVYVALERACRSVLHLHAPSEAPQIVRGASDARKHTYLTIAWRM-- 127
OY 157 GDGEDKXCPYIKREYECGDVQLLSCAVQSAQMVAVDYVPTLVSRNGAGLTIFSPA 216
Db 128 ---GDNCALPITVWEYTECPYKNSLGVCPTRQPRNSY-YDSFSAVSEDLGFLMAHAPAF 183
OY 217 ALSGOYLLTKIGFNAQTALVTLFVNDRC-LKIGSQLNPLPSKWTTEYOYQTFQGHLY 275
Db 184 ETAGTYRLVKINDWETITQFLEHRAKSCYALPLRIPACLTSKAYQOGVTVDSIG 243
OY 276 PIADYTRHADVDYRGYEDILQRMNNLLRKKNPSADPPRDSVPOEIPAVT-----KKAEG 331
Db 244 ML-----PRFIPENQRTVALYSKIAGW 266
OY 332 RTPDAESSEKKAPPESEDDMQAEASGENPALPEDEVEDTE-HDDP-----NSDP 384
Db 267 HGKRPYTLTLPELSD-----TTNATQPELPEPD---PEDSALLEDPAGTVSSQIIPN 318
OY 385 YYNDMPAVIPV---EETKSSNAVSMFFAFAVCAVALVGLVW 426
Db 319 WH--IPSIDVAPNHNAAPARNPGLITGALAGSTALVALTIGIAW 362

RESULT 9
E43674
US6 Protein - human herpesvirus 2 (strain H652)
C:Species: human herpesvirus 2
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: E43674
R:McGeoch, D.J.; Moss, H.W.M.; McNab, D.; Frame, M.C.
J. Gen. Virol. 68, 19-38, 1987
A:Title: DNA sequence and genetic content of the HindIII 1 region in the short unique
nucleonary comparisons.
A:Reference number: A43674; MUID:87111457; PMID:3027242
A:Accession: E43674
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-393 <MC>
A:Cross-References: EMBL:X04798
C:Superfamily: herpesvirus glycoprotein D

Query Match 6.8%; Score 158; DB 2; Length 393;
Best Local Similarity 20.3%; Pred. No. 0.00014;
Matches 71; Conservative 53; Mismatches 148; Indels 78; Gaps 13;

OY 97 DALTPAVGPNRYLTRSRGCDVVELNPISNVDNISAKEREKGPFEASVWFYVYK 156
Db 71 DFPQPSI-PTTYVYVALERACRSVLHLHAPSEAPQIVRGASDARKHTYLTIAWRM-- 127
OY 157 GDGEDKXCPYIKREYECGDVQLLSCAVQSAQMVAVDYVPTLVSRNGAGLTIFSPA 216
Db 128 ---GDNCALPITVWEYTECPYKNSLGVCPTRQPRNSY-YDSFSAVSEDLGFLMAHAPAF 183
OY 217 ALSGOYLLTKIGFNAQTALVTLFVNDRC-LKIGSQLNPLPSKWTTEYOYQTFQGHLY 275
Db 184 ETAGTYRLVKINDWETITQFLEHRAKSCYALPLRIPACLTSKAYQOGVTVDSIG 243
OY 276 PIADYTRHADVDYRGYEDILQRMNNLLRKKNPSADPPRDSVPOEIPAVT-----KKAEG 331
Db 244 ML-----PRFIPENQRTVALYSKIAGW 266
OY 332 RTPDAESSEKKAPPESEDDMQAEASGENPALPEDEVEDTE-HDDP-----NSDP 384

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OY 348 S 348  
Db 345 S 345

## RESULT 13

Probable glycoprotein D - equine herpesvirus 4 (strain NS80567)

C:Species: equine herpesvirus 4

A:Virus: strain NS80567

C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 21-Jul-2000

R:Telord, E.A.; Watson, M.S.; Perry, J.; Cullinane, A.A.; Davison, A.J.

J. Gen. Virol. 79, 1197-1203, 1998

A:Title: The DNA sequence of equine herpesvirus-4.

A:Reference number: 222173; MUID:98264497; PMID:9603335

A:Accession: T42615

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-402 <TEL>

A:Cross-references: EMBL:AF030027; NID:g2605950; PIDN:ACG59592.1; PID:g2606020

A:Experimental source: strain NS80567

C:Genetics:

A:Note: 72

C:Superfamily: herpesvirus glycoprotein D

Query Match

Best Local Similarity 22.3%; Score 146; DB 2; Length 402;

Matches 67; Conservative 38; Mismatches 120; Indels 76; Gaps 13;

OY 94 RAIDLALIPANGPYNRILTRVSCDYLNPISNDVMTSAKEKEGPFASVWFY 153

Db 75 KIYDVKTVAATRP-----CEMALIALAKTNVDSIIKELDAHK--TYSARLTWFK 121

OY 154 VIKGDDEDEKXC--PIYKREYREGCDVQLSECAVOSQAMAVDYVSTLVSRGAGLTI 211

Db 122 I-----PTCATPIHDVYVMCMKPRLLFGMCDERINILMTTAAETDDELGLVL 174

OY 212 FSPFAASGOYLTLTKI-GPFAQTALVTLVNDRCIKIGSOLNF-LPSKQWTEYOYTG- 268

Db 175 ASPAHSTYGLYRVLQIDGRRIYDFSVTIPSSHC-PLSFQNFNGNDRCCKTEQYSRGE 233

OY 269 -----FOGELH-----YPLADTNTTRADVDYRG 291

Db 234 VYNSRFLSEPNYQGVHLAVKWFVQDGNLFVQTEAQAFAFPVPDPDHPGDSV--- 290

OY 292 YEDIIORWNNLLRKKNSAPDPRP---DSVPOEIPAVTKKAGRTPDASSESKKAPPD 347

Db 291 ESEITONKTN--PKQEQASPKPMPRPKWPSPKQIAPRIDEVDNAK---EITTKKPPASN 344

OY 348 S 348

Db 345 S 345

## RESULT 14

glycoprotein D precursor - bovine herpesvirus 1 (strain P8-2)

C:Species: bovine herpesvirus 1

C:Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 16-Jul-1999

C:Accession: A36548

R:Tiiko, S.K.; Fitzpatrick, D.R.; Babluk, L.A.; Zamb, T.J.

J. Virol. 64, 5132-5142, 1990

A:Title: Molecular cloning, sequencing, and expression of functional bovine herpesvirus

A:Reference number: A36548; MUID:90376470; PMID:2168991

A:Accession: A36548

A:Molecule type: DNA

A:Residues: 1-417 <TIK>

A:Cross-references: GB:M59846; NID:g330745; PIDN:AAA46050.1; PID:g330746

C:Superfamily: herpesvirus glycoprotein D

C:Keywords: glycoprotein; transmembrane protein

F:1-19/DNA: signal sequence #status predicted <SIG>

F:20-417/Product: glycoprotein D #status predicted <NAT>  
F:361-369/Domain: transmembrane #status predicted <TMN>  
F:41/102/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 23.1%; Score 144; DB 1; Length 417;

Matches 79; Conservative 47; Mismatches 156; Indels 60; Gaps 17;

OY 109 RYLTVRSRGCDVVELNPISNVDMISAKEKEGPFASVWFYIKGDGDEKXC--P 166

Db 67 RYATSA-AACDMLALINDPQVGRITLMEAVRRH--ARAVNATVIMYKIESG-----CARP 117

OY 167 IYKREYREGCDVQLSECAVOSQAMAVDYVSTLVSRNAGLTIPTAALSGOYLTL 226

Db 118 LYVMEITECEPKRKFQICRTPTPEFWSFLAGRAYPTDDELGLIMAPARLVGOYRRAL 177

OY 227 KI-GPFAQT-ALVTLVNDRC--LKIGSOLNLFPSKQWTEYOYQ-----TGF--Q 270

Db 178 YIDGTVAYTDFVNSLPAGD-CWFSKLGANGYTFGACFPARQVEQKVLRLTYLTQYRQ 236

OY 271 GEHLYPIADTNTTRADVDY-----YKGYEDIIORWNNLLRKKNSAPDPRPSVPOEIPA 324

Db 237 EAHKATVDYWMRHRGGVPPYFEESKGYE-----PPADGSGPAPPGDDDA 283

OY 325 VTKKAEGRPD-AESSKKAPPEDESDDMQEAASGENPALPEDEDEVEDTEHDNSD- 382

Db 284 --REDEGETEDGAAGREGNGCPGPGDGSQTPPEANGAGEGPKRP-----SPDAOR 335

OY 383 PDYVNDMPAVI---PVEETTKSSNAYSMPIFAFAVCAVALV 421

Db 336 PEGWPSLEAITHPAPATPAADPAADPAVSGIGIAAALACV 377

## RESULT 15

glycoprotein gD - bovine herpesvirus 1

C:Species: bovine herpesvirus 1

C:Date: 09-Jun-1994 #sequence\_revision 12-May-1995 #text\_change 26-Aug-1999

C:Accession: S35784

R:Audonnet, J.

submitted to the EMBL Data Library, June 1993

A:Reference number: S35782

A:Accession: S35784

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-417 <AUD>

A:Cross-references: EMBL:Z23068; NID:g312185; PIDN:CAA80604.1; PID:g312188

C:Superfamily: herpesvirus glycoprotein D

C:Keywords: glycoprotein

Query Match

Best Local Similarity 22.2%; Score 139.5; DB 2; Length 417;

Matches 88; Conservative 41; Mismatches 179; Indels 89; Gaps 16;

OY 58 MDRHLFLRNAEWTIVLSSFSQSTAAVYDYILGRRLDALITPANGPYNRILTVSRG 117

Db 37 MPRVNYTERMHTTGPISPFPADGREGQPEVNRASAAACDMLALINDPQVGRITLMEAVR- 95

OY 118 CDVVELNPISNVDMISAKEKEGPFASVWFYIKGDGDEKXC--PIYKREYREC 175

Db 96 -----RHARAVNATVIMYKIESG-----CARPLYMEYTEEC 126

OY 176 GDVQLSECAVOSQAMAVDYVSTLVSRNAGLTIPTAALSGOYLTLTKI-GPFAQT 234

Db 127 EPRKHEGCRKRTPTPEFWSFLAGRAYPTDDELGLIMAPARLVGOYRRALYIDGTVAYT 186

OY 235 -ALVTLVNDRC--LKIGSOLNLFPSKQWTEYOYTGFGGELH-----YF-----I 277

Db 187 DFMWILPAGD-CWFSKLGANGYTFGACFPAREX-----QNKVLLALTYLTQYRQEAHAI 242

OY 278 AD-INTTRADVDY-----YKGYEDIIORWNNLLRKKNSAPDPRPSVPOEIPATKAE 330

Db 243 VDIWMRHRGGVPPYFEESKGYE-----PPAADG-----GSPAPGDDE 282



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Db      85  RVERACSVLLNAPSEARQIIRGASSEDYRKRPYUMLTAMFM-----GCNALPITVMEY 139
QY      173  RECGVOLLISCAVQASQAMAVDVYPS- TLVSRNAGUUIFSPALSGUYLLTIKIGRF 231
      || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      140  TECSTYNSLGCAPRTQPRW--NYYDSFAASEDNELFELHMAPAFETAGTYLRLVKINDM 197
QY      232  AQTALVLTLE--VNDRCLTIGSQLNLFPSKCWTJDOYGT-----FOGEHLXPIA 278
      || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      198  TEITQFILEHRAKQSC-KYTLPLRPIPSACLSRQAYQGYVDSIGMLPRFIREMNORTVA 256
QY      279  DFNRRHADDDYRKGEDILQRRNNLLRKKNSAPDRPDSVQETPRAVTKRAEGRTDAES 338
      || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      257  VYSKIKG-----WH-----GRRAP-YTSTLLRPETL-----ETPNA-- 287
QY      339  SEKKAPDESEDD--MQAEASGENFALPEDEDEVELETHNDPMSDPRYNDMAVYRVEE 397
      || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      288  TOPELADEDEDSALLIEDPYGTVAQRIPRMWHIRISIDATGRIHPRATPRNMGLT----- 342
QY      398  TTKSNAVSMPIFAAFVACAVLAVGLLLW 426
      || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      343  -----AGAVGSLALALVTC-----GIYVW 362

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ID	VGID_HSV11	STANDARD;	PRT;	394 AA.
OC	069091;	P03171; 012833; 012544;		
DT	21-JUL-1986	(Rel. 01, Created)		
DT	16-OCT-2001	(Rel. 40, Last sequence update)		
DT	16-OCT-2001	(Rel. 40, Last annotation update)		
DE	Glycoprotein D precursor.			
GN	GD OR US6.			
OS	Herpes simplex virus (type 1 / strain 17).			
OC	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;			
OC	Alphaherpesvirinae; Simplexvirus.			
OX	NCBI_TaxID=10299;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=85160822; PubMed=2984429;			
RA	McGeoch D.J., Dolan A., Donald S., Rixon F.J.;			
RT	"Sequence determination and genetic content of the short unique region			
RT	in the genome of herpes simplex virus type 1.";			
RL	J. Mol. Biol. 181:1-13(1985).			
RL	[2]			
RP	REVIEWS.			
RA	McGeoch D.J.;			
RL	Submitted (JAN-1989) to the EMBL/Genbank/DBJ databases.			
CC	-1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1: GH,			
CC	GB, GC, GD, GI, AND GE.			
CC	-1- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN D FAMILY.			
CC	-----			
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CC	or send an email to <a href="mailto:license@sdb-sdb.ch">license@sdb-sdb.ch</a> .			
CC	-----			
DR	EMBL; L00036; AAA9682.1; -			
DR	EMBL; X14112; CAA32283.1; -			
DR	PIR; A03730; VGBEL7.			
DR	InterPro; IPR002896; Herpes_glycop_D.			
DR	Pfam; PF01537; Herpes_glycop_D; 1.			
KW	Glycoprotein; Transmembrane; Signal.			
FT	SIGNAL	1	25	POTENTIAL.
FT	CHAIN	26	394	GLYCOPROTEIN D.
FT	DOMAIN	26	339	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	340	364	POTENTIAL.
FT	DOMAIN	365	394	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	365	381	ARG/LYS-RICH (HIGHLY BASIC; PROBABLY
FT				SERVES TO ANCHOR THE GLYCOPROTEIN IN
FT				THE MEMBRANE).

FT	CARBOHYD	119	119	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	146	146	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	287	287	N-LINKED (GLCNAC. . .)	(POTENTIAL)
SO	SEQUENCE	394 AA;	43346 MM;	94BS2171P35576FC	CRC64;

Query Match	8.28;	Score 190;	DB 1;	Length 394;
Best Local Similarity	23.28;	Pred. No. 4.5e-07;		
Matches 78;	Conservative 47;	Mismatches 145;	Indels 66;	Gaps 14;

```

QY 106 PNRNLTFRSRBCDVEELNPLSNDDMTISAKEREKGFPAASVYVYV1KGDGDEKRC 166
Db 79 P1TVYVAVLERACRSVLLNABSEAPQ1YRGASEDVROPYMLLT1TAMFRM-----GGNCAl 133
QY 166 P1YKREYRCBGDVL1LSECAVQASOMAVADVPS-T1VSRNAGLTFSP1ALSGOYL 224
Db 134 P1TVMEYECYSYKSLGACPIRTOPRW--NYDSFSAVSEDNLCGLMHAAPAFETAGYTLR 191
QY 225 TLK1RFPOTALVLTLE--VNDRC1K1SSQLF1PSKCTTQYQYTG-----FQG 271
Db 192 LVK1NDW1E1TQF1L1EHNAKSSC-KYALPL1P1PSAC1SPQAVQOGTVDS1GMLPR1P 256
QY 272 EHL1P1AD1NTRHADVDYRGYED1LQRMN1N1LRKKNBSAPDRPDSVPOE1PAVTYKRAEG 331
Db 251 ENQRTAVAY1SK1K1G-----WH-----GKRA1-YTST1LP1EL-----S 283
QY 332 RTPDAESSEKAPPEDESD-MQAEASGENP1ALPEDEDEVPEDETHNDPMSDPDYKNDP 390
Db 284 ETPMA--TQPLAR1EDPDESD1LLEDPGY1APQ1P1P1W1H1P1SD0A1TP1H1P1AT1P1NMG 341
QY 391 AV1VEE1ETKSN1N1AP1P1AF1Y1AC1VAL1GL1W 426
Db 342 L1-----AGAVGSL1AL1V1TC-----G1Y1W 363

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RESULT 3	VGID_HSV1P	STANDARD;	PRT;	394 AA.
ID	VGID_HSV1P			
AC	P57083; P03171;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Glycoprotein D precursor.			
GD	OR 056.			
OS	Herpes simplex virus (type 1 / strain Patton).			
OC	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;			
OC	Alphaherpesvirinae; Simplexvirus.			
OX	NCBI_TaxID=10308;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE-83016630; PubMed=6289440;			
RX	Watson R.J., Weiss J.H., Salstrom J.S., Engquist L.W.;			
RT	"Herpes simplex virus type-1 glycoprotein D gene: nucleotide sequence and expression in Escherichia coli."			
RL	Science 218:381-384(1982).			
CC	-1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1: GH, GB, GC, GD, GI, AND GE.			
CC	-1- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN D FAMILY.			
CC	-----			
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CC	-----			
EMBL	X02138; CAA26060.1; -			
DR	EMBL; J02217; AAA45785.1; -			
DR	PIR; A03729; VGBED1.			
DR	InterPro; IPR002896; Herpes_glycop-D.			
DR	Pfam; PF01537; Herpes-glycop_D; 1.			
DR	Glycoprotein; Transmembrane; Signal.			
RT	SIGNAL			
	1			
	25			
	POTENTIAL.			



FT CHAIN 26 394 GLYCOPROTEIN D.  
 FT DOMAIN 26 339 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 340 364 POTENTIAL.  
 FT DOMAIN 365 394 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 365 381 ARG/LYS-RICH (HIGHLY BASIC; PROBABLY  
 SERVES TO ANCHOR THE GLYCOPROTEIN IN  
 THE MEMBRANE).  
 FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 394 AA; 43346 MW; 052ABB5F5303D5E CRC64;

Query Match 8.2%; Score 190; DB 1; Length 394;  
 Best Local Similarity 23.2%; Pred. No. 4.5e-07;  
 Matches 78; Conservative 47; Mismatches 145; Indels 66; Gaps 14;

DB 106 PYNRYLTRVSRGCDVVELNPISNVDMSIAAKEKEGPFEPASVYWFYIKDGEDKCYC 165  
 79 PITVYVAVLERACRSVLLNAPSEAPQIVRGASEDVRKQPNULTIAMFRM-----GCNCAI 133  
 QY 166 PIYKREYREGCDVOLLSECAVQSQMMAVDYVPS-TLYSRNGAGLITISPTAALSGOYL 224  
 134 PITVMEYTECSYNSKSLGACPIRTQPRW--NYDSFSAVSEDLGFLMAHPAFETAGTYLR 191  
 DB 225 TLKIGRFAQTALVLTLE--VNDRCCLKIGSQLNPLPSKWTBOYQFG-----FQG 271  
 192 LKIKNDWETITQFLIENHAKGSC-KYALPLRIPPSACLSPOAYQGVVDSIGMLPRIP 250  
 QY 272 EHLPIADTNRHADVDYRGYEDILQRMNNLLRKNPSAPDRPDSVPOEIPAVTKKAEG 331  
 251 ENQGTAVVYSLKING-----WH-----GPKAP-YTSTLLPEL-----S 283  
 QY 332 RTPAESSEKAPDESDD-MQAEASGENPALPEDDEVEDTEHDDPNSDPYNNMP 390  
 284 ETPNA--TQPELAPDEPDSALLEDVGTVAQIIPNMHIPSIDAAATPHHPATPNMG 341  
 QY 391 AVIPEETTKSSNAVSMPIFAFVACAVALLVLMW 426  
 DB 342 LI-----AGAVGSLALALVYC-----GIYVW 363

RESULT 4  
 VGLD\_HSV1A STANDARD; PRT; 394 AA.  
 ID VGLD\_HSV1A STANDARD; PRT; 394 AA.  
 AC P36318; 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Glycoprotein D precursor.  
 GN GP OR US6.  
 OS Herpes simplex virus (type 1 / strain Angelotti).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Simplexvirus.  
 OX NCBI\_TaxID=10301;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90324869; PubMed=2165127;  
 RA Isumi K.M., Stevens J.G.;  
 RT "Molecular and biological characterization of a herpes simplex virus  
 type 1 (HSV-1) neuroinvasiveness gene.";  
 RT J. Exp. Med. 172:487-496(1990).  
 CC -1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1: GH,  
 CC -1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1: GH,  
 CC GB, GC, GG, GD, GI, AND GE.  
 CC -1- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN D FAMILY.  
 CC -1- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN D FAMILY.  
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DR EMBL: X54361; CAA38245.1; -.  
 DR PIR: A47627; A47627.  
 DR InterPro: IPR02896; Herpes-glycop\_D.  
 DR Pfam: PF01537; Herpes-glycop\_D; 1.  
 DR GlycoProtein; Transmembrane; Signal.  
 FT SIGNAL 1 25  
 FT CHAIN 26 394 GLYCOPROTEIN D.  
 FT DOMAIN 26 339 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 340 364 POTENTIAL.  
 FT DOMAIN 365 394 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 365 381 ARG/LYS-RICH (HIGHLY BASIC; PROBABLY  
 SERVES TO ANCHOR THE GLYCOPROTEIN IN  
 THE MEMBRANE).  
 FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 394 AA; 43303 MW; 47DE3BC79BB28950 CRC64;

Query Match 8.1%; Score 187; DB 1; Length 394;  
 Best Local Similarity 23.5%; Pred. No. 7.6e-07;  
 Matches 77; Conservative 46; Mismatches 155; Indels 50; Gaps 14;

DB 106 PYNRYLTRVSRGCDVVELNPISNVDMSIAAKEKEGPFEPASVYWFYIKDGEDKCYC 165  
 79 PITVYVAVLERACRSVLLNAPSEAPQIVRGASEDVRKQPNULTIAMFRM-----GCNCAI 133  
 QY 166 PIYKREYREGCDVOLLSECAVQSQMMAVDYVPS-TLYSRNGAGLITISPTAALSGOYL 224  
 134 PITVMEYTECSYNSKSLGACPIRTQPRW--NYDSFSAVSEDLGFLMAHPAFETAGTYLR 191  
 DB 225 TLKIGRFAQTALVLTLE--VNDRCCLKIGSQLNPLPSKWTBOYQFG-----LYPIAD 279  
 192 LKIKNDWETITQFLIENHAKGSC-KYALPLRIPPSACLSPOAYQGVVDSIGMLPRIP 250  
 QY 280 TNRHADVDYRGYEDILQRMNNLLRKNPSAPDRPDSVPOEIPAVTKKAEGRPDAESS 339  
 251 ENQ-----IVAVYSLKINGMH-----GPKAP-YTSTLLPEL-----SETPNA--T 289  
 DB 340 EKKAPPEDESDD-MQAEASGENPALPEDDEVEDTEHDDPNSDPYNNMP 398  
 290 QPELAPDEPDSALLEDVGTVAQIIPNMHIPSIDAAATPHHPATPNMG 343  
 QY 399 TKSSNAVSMPIFAFVACAVALLVLMW 426  
 DB 344 ---AGAVGSLALALVYC-----GIYVW 363

RESULT 5  
 VGLD\_HSV1E STANDARD; PRT; 442 AA.  
 ID VGLD\_HSV1E STANDARD; PRT; 442 AA.  
 AC P22484; 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Glycoprotein D precursor (Glycoprotein 17/18).  
 GN GP OR GP17/18 OR 72.  
 OS Equine herpesvirus type 1 (strain Kentucky A) (EHV-1).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Varicellovirus.  
 OX NCBI\_TaxID=10329;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91082407; PubMed=1845821;  
 RA Flowers C.C., Eastman E.M., O'Callaghan D.J.;  
 RT "Sequence analysis of a glycoprotein D gene homolog within the unique  
 RT short segment of the EHV-1 genome.";  
 RT Virology 180:175-184(1991).  
 RN 12  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92263758; PubMed=1316673;  
 RA Colle C.F., III, Flowers C.C., O'Callaghan D.J.;  
 RT "Open reading frames encoding a protein kinase, homolog of  
 RT glycoprotein gx of pseudorabies virus, and a novel glycoprotein map

RT within the unique short segment of equine herpesvirus type 1.";  
 RL Virology 188:545-557(1992).  
 CC -1- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN D FAMILY.  
 CC -----  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch))  
 CC -----  
 DR EMBL: M62923; AAA46081.1; -  
 DR EMBL: M86931; NOT\_ANNOTATED\_CDS.  
 DR EMBL: M87497; AAA46073.1; ALT\_INIT.  
 DR PIR: A38518; VGBBEA.  
 DR InterPro: IPR002896; Herpes\_glycop\_D.  
 DR Pfam: PF01537; Herpes\_glycop.D; 1.  
 KW Glycoprotein; Signal; Transmembrane.  
 FT SIGNAL 1 19  
 FT CHAIN 20 442  
 FT DOMAIN 20 405  
 FT TRANSMEM 406 422  
 FT DOMAIN 423 442  
 FT CARBOHYD 103 103  
 FT CARBOHYD 111 111  
 FT CARBOHYD 347 347  
 FT CARBOHYD 396 396  
 SQ SEQUENCE 442 AA; 49908 MW; 323CDA9C9762F05 CRC64;  
 -----  
 Query Match 7.8%; Score 181; DB 1; Length 442;  
 Best Local Similarity 23.0%; Pred. No. 2, 5e-06;  
 Matches 84; Conservative 56; Mismatches 153; Indels 72; Gaps 17;  
 QY 87 YDY-ILGRALDALTIPAVGP-----YNNRYLTRVSRGCDVLENPISNVDMISAKEK 141  
 DB 102 YNNYILTRYNATALASPFINDQVKNVDLRIYATRPCEMIALIAKTINDSLKELAAOK 161  
 QY 142 GGPFEASVWVFYIKGDDGDEKVC--PIYKREYREGCDVOLLSECAVOSQOMAVDYVPS 199  
 DB 162 --TYSARLTWFKIM-----PTCATPIHDVSYMKCNPKLSFAMCDERSDILMQASLITM 212  
 QY 200 TLVSRNAGLTIFSPALSGOYLTLTKI--GFAQTALVLEVNDRCLKISQOLF--LPS 257  
 DB 213 AAEFDDELGLVLAAPAHSAHSGLYRVIETDGRRIYDFSVTISERC--PIAFELNENPD 271  
 QY 258 KCMTEYOYGTG-----FQGEHLVPIADTNTIRAD-----DYRYGEDILLQRRNNILRK 306  
 DB 272 RCKTPEQYSRGEVFTRRRLGEFNFQGE-----HMTWKFWFVYDG--GNLPVQFEAQAFA 326  
 QY 307 NPSAPDPRP--DSVPOELIPAVTKKAEGRTPDAESSEKKAPPESEDDMQAEASGENPA-- 362  
 DB 327 RVPRPDHPGDSVESLI-----TQNKTDPKPGQADPKPNQPFKNSIK 370  
 QY 363 -ALPEDDEVPEDEHDPNSDPDYNDMPAVIPEEETKSSNAVSPIFAFAACVAVLY 421  
 DB 371 HAVPRLEDEVIE-----PYTKPPK--TSSNSTFVGISVGLGIAVLV 414  
 QY 422 GLIWM 426  
 DB 415 GVILY 419  
 -----  
 RESULT 6  
 VGLD\_HSVEA  
 AC P24872; STANDARD; PRT; 402 AA.  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Glycoprotein D precursor (glycoprotein 17/18).  
 GN GD OR GP17/18 OR 72.  
 OS Equine herpesvirus type 1 (strain Ab1) (EHV-1).

CC Viruses: dsDNA viruses, no RNA stage: Herpesviridae;  
 CC Alphaherpesvirinae; Varicellovirus.  
 OX NCBI\_TaxID=10328;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92268882; PubMed=1316942;  
 RA Elton D.M., Halliburton I.W., Killington R.A., Meredith D.M.,  
 RA Bonass W.A.;  
 RT "Identification of the equine herpesvirus type 1 glycoprotein 17/18  
 RT as a homologue of herpes simplex virus glycoprotein D.";  
 RL J. Gen. Virol. 73:1227-1233(1992).  
 RN [2]  
 RP SEQUENCE OF 242-402 FROM N.A.  
 RX MEDLINE=91276272; PubMed=1647359;  
 RA Elton D.M., Halliburton I.W., Killington R.A., Meredith D.M.,  
 RA Bonass W.A.;  
 RT "Sequence analysis of the 4.7-kb BamHI-EcoRI fragment of the equine  
 RT herpesvirus type-1 short unique region.";  
 RL Gene 101:203-208(1991).  
 CC -1- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN D FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: M60946; AAA46087.1; -  
 DR EMBL: M36299; AAA66546.1; -  
 DR PIR: P00146; P00146.  
 DR InterPro: IPR002896; Herpes\_glycop\_D.  
 DR Pfam: PF01537; Herpes\_glycop.D; 1.  
 KW Glycoprotein; Transmembrane; Signal.  
 FT SIGNAL 1 30  
 FT CHAIN 31 402  
 FT DOMAIN 31 355  
 FT TRANSMEM 356 372  
 FT DOMAIN 373 402  
 FT CARBOHYD 53 53  
 FT CARBOHYD 61 61  
 FT CARBOHYD 297 297  
 FT CARBOHYD 346 346  
 SQ SEQUENCE 402 AA; 45211 MW; 78A0593232D0238C CRC64;  
 -----  
 Query Match 7.6%; Score 175; DB 1; Length 402;  
 Best Local Similarity 22.6%; Pred. No. 6, 2e-06;  
 Matches 84; Conservative 53; Mismatches 149; Indels 86; Gaps 17;  
 QY 87 YDY-ILGRALDALTIPAVGP-----YNNRYLTRVSRGCDVLENPISNVDMISAKEK 141  
 DB 52 YNNYILTRYNATALASPFINDQVKNVDLRIYATRPCEMIALIAKTINDSLKELAAOK 111  
 QY 142 GGPFEASVWVFYIKGDDGDEKVC--PIYKREYREGCDVOLLSECAVOSQOMAVDYVPS 199  
 DB 112 --TYSARLTWFKIM-----PTCATPIHDVSYMKCNPKLSFAMCDERSDILMQASLITM 162  
 QY 200 TLVSRNAGLTIFSPALSGOYLTLTKI--GFAQTALVLEVNDRCLKISQOLF--LPS 257  
 DB 163 AAEFDDELGLVLAAPAHSAHSGLYRVIETDGRRIYDFSVTISERC--PIAFEQNGFND 221  
 QY 258 KCMTEYOYGTG-----FQGEHLVPIADTNTIRADVRYGEDILLQRRNNILRK 305  
 DB 222 RCKTPEQYSRGEVFTRRRLGEFNFQGEHMT-----WTKFWFVYDGGILPVQF 269  
 QY 306 -----KNPSAPDPRP--DSVPOELIPAVTKKAEGRTPDAESSEKKAPPESEDDMQAEAS 357  
 DB 270 YEAQAFAPVPDHPGDSVESLI-----TQNKTDPKPGQADPKPNQPFKNSIK 313  
 QY 358 GENPA--ALPEDDEVPEDEHDPNSDPDYNDMPAVIPEEETKSSNAVSPIFAFAV 414  
 DB 314 FKWPSIKHLARLDEVIE-----PYTKPPK--TSSNSTFVGISVGLG 357

OY 415 ACAVALGLVW 426  
Db 358 IAGLVGVILY 369

## RESULT 7

VGLD\_HSVB STANDARD; PRT; 452 AA.

AC P24379;  
DT 01-MAR-1992 (Rel. 21, Created)  
DT 01-MAR-1992 (Rel. 21, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Glycoprotein D precursor (Glycoprotein 17/18).  
GN GP OR GP17/18 OR 72.  
OS Equine herpesvirus type 1 (strain Ab4p) (EHV-1), and  
OS Equine herpesvirus type 1 (strain Kentucky D) (EHV-1).  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Alphaherpesvirinae; Varicelloviruses.  
NCBI\_TaxID=31520, 10330;

SEQUENCE FROM N.A.

STRAIN-AB4P;

RC MEDLINE=92295566; PubMed=1318606;

RA Telford E.A.R., Watson M.S., McBride K., Davison A.J.;

RT "The DNA sequence of equine herpesvirus-1.";

RL Virology 189:304-316(1992).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Kentucky D;

RX MEDLINE=91108393; PubMed=2177089;

RA Audonnet J.-C., Winslow J., Allen G., Paolletti E.;

RT "Equine herpesvirus type 1 unique short fragment encodes

RT glycoproteins with homology to herpes simplex virus type 1 gp, g1 and

RT 9E.";

RL J. Gen. Virol. 71:2969-2978(1990).

CC -1- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN D FAMILY.

CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-51 IS THE INITIATOR.

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL: M86664; AAB02507.1;

DR PIR: I36802; VGBEG3.

DR PIR: B36646; VGBEEV.

DR InterPro: IPR002896; Herpes\_glycop\_D.

DR Pfam: PF01537; Herpes\_glycop\_D.1.

CC Glycoprotein: Signal; Transmembrane.

FT SIGNAL 1 19 POTENTIAL.

FT CHAIN 20 452 GLYCOPROTEIN D.

FT DOMAIN 20 405 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 406 422 POTENTIAL.

FT DOMAIN 423 452 CYTOPLASMIC (POTENTIAL).

FT CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 347 347 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).

Query Match 7.6%; Score 175; DB 1; Length 452;  
Best Local Similarity 22.6%; Pred. No. 7.3e-06;  
Matches 84; Conservative 53; Mismatches 149; Indels 86; Gaps 17;

OY 87 YDY-ILGRALDLITPAVGP---YNRYLTRVSGGVVLELNPISVNDMISAAREK 141  
Db 102 YNVTILTRYNATLALSPFINDQVNDLRIVTATRPCEMIALIAKTINDSIDLKEIAAOK 161  
OY 142 GGFEASVWVFYIKGDGDKYC--PIYRKEKRGCDVLLSECAVQSQMNAVDYVPS 199

Db 162 --TYSARLTWFKIM-----PFCATPIHDVSYKNCNPKLSFAACDERSDILMQASLITM 212  
OY 200 TLVSRNGAGLTIFSPALSGQYLLTKT-GRFAOTALVTEVNDRLKIGSQINL-LPS 257  
Db 213 AAFTEDELGLVLAAPAHASGLYRRVIEIDRRITVDFSVYIPSEK-PIAFEQNFQNP 271  
OY 258 KCMTEBOYONG-----FQGHLYPIADTNRHADVDYRGREDLQW-----NNLRK- 305  
Db 272 RCKTPEQYSRGEVTRRRLGFEFPGGEHMT-----WLKFWYDGNLGVQF 319  
OY 306 -----KNPSADPRP--DSVPOEIPAVTKAEGRTDAESSEKAPDESDMQAEAS 357  
Db 320 YEAQAFARPPVPPDHHPGDSVSEI-----TQKTPPKPGQADPKRNQ 363  
OY 358 GENPA--ALPEDEVEDTEHDDNSDPDYNDMPAVIYEETTKSSNAVSMIFAFAV 414  
Db 364 FKWPSIKHLAPRLDEVEVIE-----PVTKPKK--TSKSNSTFVGISVGLG 407  
OY 415 ACAVALGLVW 426  
Db 408 IAGLVGVILY 419

## RESULT 8

VGLD\_PVRRI STANDARD; PRT; 402 AA.

AC P07645;

DT 01-APR-1988 (Rel. 07, Created)

DT 01-APR-1988 (Rel. 07, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Glycoprotein GP50.

OS Pseudorabies virus (strain Rice) (PRV).

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

OC Alphaherpesvirinae; Varicelloviruses.

NCBI\_TaxID=10350;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=86281819; PubMed=3016293;

RA Petrovskis E.A., Timmins J.G., Armentrout M.A., Marchionni C.C.,

RA Vancey R.J., Jr., Post L.E.;

RT "RNA sequence of the gene for pseudorabies virus gp50, a glycoprotein

RT without N-linked glycosylation.";

RL J. Virol. 59:216-223(1986).

CC -1- MISCELLANEOUS: GLYCOPROTEIN GP50 DOES NOT CONTAIN N-LINKED

CC CARBOHYDRATE, AS PREDICTED FROM ITS SEQUENCE.

CC -1- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN D FAMILY.

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CC EMBL: M14001; AAC35203.1;

DR PIR: A27788; VGBE50.

DR InterPro: IPR002896; Herpes\_glycop\_D.

DR Pfam: PF01537; Herpes\_glycop\_D.1.

CC Glycoprotein.

FT SIGNAL 402 AA; 44501 MW; B8763305995871E8 CRC64;

FT SIGNAL 402 AA; 44501 MW; B8763305995871E8 CRC64;

FT SIGNAL 402 AA; 44501 MW; B8763305995871E8 CRC64;

FT SIGNAL 402 AA; 44501 MW; B8763305995871E8 CRC64;

FT SIGNAL 402 AA; 44501 MW; B8763305995871E8 CRC64;

FT SIGNAL 402 AA; 44501 MW; B8763305995871E8 CRC64;

FT SIGNAL 402 AA; 44501 MW; B8763305995871E8 CRC64;

FT SIGNAL 402 AA; 44501 MW; B8763305995871E8 CRC64;

FT SIGNAL 402 AA; 44501 MW; B8763305995871E8 CRC64;

FT SIGNAL 402 AA; 44501 MW; B8763305995871E8 CRC64;

FT SIGNAL 402 AA; 44501 MW; B8763305995871E8 CRC64;

FT SIGNAL 402 AA; 44501 MW; B8763305995871E8 CRC64;

FT SIGNAL 402 AA; 44501 MW; B8763305995871E8 CRC64;

FT SIGNAL 402 AA; 44501 MW; B8763305995871E8 CRC64;

FT SIGNAL 402 AA; 44501 MW; B8763305995871E8 CRC64;

FT SIGNAL 402 AA; 44501 MW; B8763305995871E8 CRC64;

FT SIGNAL 402 AA; 44501 MW; B8763305995871E8 CRC64;

Query Match 7.1%; Score 165; DB 1; Length 402;  
Best Local Similarity 21.0%; Pred. No. 3.5e-05;  
Matches 88; Conservative 55; Mismatches 159; Indels 118; Gaps 19;

OY 73 LLSFASQSTAAVYDIILG-----RRALDLITPAVGPVRYLTR-VSRG 117  
Db 6 LLALVALRTLLGADVDAVPAFPFPAYPYTESQWLTTLTFVSPFVGPADVYHTRPLEDP 65  
OY 118 CDVVELNPISVNDMISAAREKKGFEASVWVFYIKGDGDKYCP--ITRKEKREC 175

```

Db 66 CGVALLISDPOVRLNENAVARR-PTYRAHVAVYRIADG-----CAHLLEYFIEYADC 117
QY 176 GDVOLLSECAVOSAQM---AVDYPSLVLSNGGLITFSTALSCQY--LTLTKGR 230
Db 118 DPROVFGRCRRRTTPMTTPSADYFPT---EDELGLMVAAPGRNEQYRLVSVDCVN 174
QY 231 FAQALVTLVLEVNDRCLIKISQNLNPLPSKQWTEQYOTGOGHEHLYPIADTNTRHADY 288
Db 175 ILTFMVALPBGQECFPARVDQHRTYKFGACMSDSSFGRVY-----DY 217
QY 289 YR-----GYEDILGRMNNLRKKN-----PSADPRPSV 319
Db 218 MRFLTFPFQOPRHEVAVYV---YRKGRLPRHAHAATPYAIDPARPSAGSRRPRRP 273
QY 320 QEIPAVTKKAGRTPPDAESSEKAPRED-SEDDMQAASGENPALPREDDEPEDTEHDD 378
Db 274 RPRPRKPEPAPATP-----APDRLEPAPATRDHAGAGRPTRPRPRETPH-----R 320
QY 379 PNSDPDYNDMPAVI-----PVEETTKSSNAVS---MPTAAVACAVALLVGLLV 426
Db 321 PFAP-----PAVPSGWPQAPAEFPQPRPAAGVSNHRSVIGTGTAMGALLVGVCV 373

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## RESULT 9

```

ID VGLD_HSV2 STANDARD; PRT; 393 AA.
AC P03172;

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DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

```

```

DE Glycoprotein D precursor.
GN GD OR US6.

```

```

OS Herpes simplex virus (type 2).
OC Viruses: dsDNA viruses, no RNA stage; Herpesviridae;

```

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OX Alphaherpesvirinae; Simplexvirus.
NCBI_TaxID=10310;

```

```

RN SEQUENCE FROM N.A.

```

```

RA MEDLINE=84131549; PubMed=6321120;

```

```

RT "DNA sequence analysis of the type-common glycoprotein-D genes of
herpes simplex virus types 1 and 2."

```

```

RT DNA 3:23-29(1984).

```

```

RN SEQUENCE FROM N.A.

```

```

RX STRAIN=333;
MEDLINE=84159516; PubMed=6323270;

```

```

RA Watson R.J.;
"DNA sequence of the Herpes simplex virus type 2 glycoprotein D
gene."

```

```

RT gene.

```

```

RN SEQUENCE FROM N.A.

```

```

RC STRAIN=BBK;

```

```

RA Terhune S.S., Coleman K.T., Sekulovich R., Burke R.L., Spear P.G.;
Submitted (Oct-1997) to the EMBL/Genbank/DBJ databases.

```

```

CC -1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND
2: GH, GB, GC, GD, GI, AND GE.

```

```

CC -1- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN D FAMILY.

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CC EMBL; U12180; AAB60552.1; -

```

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CC EMBL; U12182; AAB60554.1; -

```

```

CC EMBL; U12183; AAB60555.1; -

```

```

CC EMBL; K02373; AAA45842.1; -

```

```

CC EMBL; K01408; AAA45841.1; -

```

```

DR EMBL; AF021342; AAB72102.1; -.
DR PIR; A03731; VGBE2.
DR PIR; A03732; VGBE3.
DR InterPro; IP002896; Herpes_glycop_D.
DR Pfam; PF01537; Herpes_glycop_D.1
KW Glycoprotein; Transmembrane; Signal.
FT SIGNAL 1 25
FT CHAIN 1 25
FT DOMAIN 26 393
FT TRANSMEM 26 393
FT DOMAIN 340 363
FT CARBOHYD 119 119
FT CARBOHYD 146 146
FT CARBOHYD 287 287
FT VARIANT 249 249
FT VARIANT 337 337
FT VARIANT 367 367
SQ SEQUENCE 393 AA; 43147 MW; A8514E21857ADEF2 CRC64;

```

```

Query Match 6.8%; Score 156.5; DB 1; Length 393;
Best Local Similarity 21.0%; Pred. No. 0.00015;
Matches 59; Conservative 50; Mismatches 137; Indels 35; Gaps 8;

```

```

QY 97 DALTPAVGPNRYLTVRSKCDVLENPISNVDWISAKEKEKGPASVWPEYVYK 156
Db 71 DPFQPSI-PIVYAVLEBRACSVLHAPSEAPQIVRASDBAKRHYTNLTIAVYRM-- 127
QY 157 GDDGEKCYPIYKKEKREGCDVQLSECAVQSAQMAVDVSTLVSRNAGLTFSPTA 216
Db 128 ---GDGCAIPVYMETTECPYKSLGVCPIRQPRVSY-YDFSFAVSEEDNLGFLHAPAF 183
QY 217 ALSGOYLTLTKIGRFAQTLVTLVENDRC-LTIGSQLNPLPSKQWTEQYOTGOGHEHLY 275
Db 184 ETAGTYLRLVYKINDMETEIQFLNHRARASCYALPLRPPACLTSAVYQGVTVDSIG 243
QY 276 PIADTNRHADYVNGEYEDILGRMNNLRKKNSAPDRP---DSVQEIYAVTKKAAG 331
Db 244 MUPRTPEP-----QRTVALYSLKTAGHNGKRPYTSITLPELSDT----- 286
QY 332 RTPDAESSEKAPREDSEDD-MQAEASGENPALPREDDEPEDV 371
Db 287 -----NATQPELVPEPDSALLEDPAGTVSSQIPPNWHIP 322

```

## RESULT 10

```

ID VGLD_HSVBP STANDARD; PRT; 417 AA.
AC P24906;

```

```

DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

```

```

DE Glycoprotein D precursor (Glycoprotein IV).
GN GD OR GIV OR US6.

```

```

OS Bovine herpesvirus type 1 (strain p8-2).
OC Viruses: dsDNA viruses, no RNA stage; Herpesviridae;

```

```

OX Alphaherpesvirinae; Varicellovirus.
NCBI_TaxID=10324;

```

```

RN SEQUENCE FROM N.A., AND SEQUENCE OF 19-48.

```

```

RA MEDLINE=90376470; PubMed=2168991;

```

```

RT "Molecular cloning, sequencing, and expression of functional bovine
herpesvirus 1 glycoprotein gIV in transfected bovine cells."

```

```

RT J. Virol. 64:5132-5142(1990).

```

```

CC -1- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN D FAMILY.

```

```

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or send an email to license@isb-sib.ch).

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CC EMBL; U12180; AAB60552.1; -

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```

CC EMBL; U12182; AAB60554.1; -

```

```

CC EMBL; U12183; AAB60555.1; -

```

```

CC EMBL; K02373; AAA45842.1; -

```

```

CC EMBL; K01408; AAA45841.1; -

```



EMBL: 223068; CAA80604.1; -  
 DR InterPro: IPR002886; Herpes\_glycop\_D.  
 DR Pfam: PF01537; Herpes\_glycop\_D.1.  
 CC Glycoprotein; Transmembrane; Signal.  
 KW SIGNAL 1 18  
 FT CHAIN 19 417 BY SIMILARITY.  
 FT DOMAIN 19 360 GLYCOPROTEIN D.  
 FT TRANSMEM 361 389 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 390 417 POTENTIAL.  
 FT CARBOHYD 41 41 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 417 AA; 45020 MW; 82E1E8757BF2DF9C CRC64;

Query Match 6.0%; Score 139.5; DB 1; Length 417;  
 Best Local Similarity 22.2%; Pred. No. 0.003;  
 Matches 88; Conservative 41; Mismatches 179; Indels 89; Gaps 16;

OY 58 MDRHLFLRNAFWTIVILSSFSASOSTAATYDYLGRRLDLTPAVGPNRYLTVRSRG 117  
 DB 37 MPRVYTERHWHTGPIPEPADGRQVPEVRYASAAACMLALADPOVGRITMEAYR- 95  
 OY 118 CDVVELANISVDDMTISAKEKEKGPEASVVEYTKGDGEDKYC--PIYREYREC 175  
 DB 96 -----RHARAYNATVIWKIESG-----CARLYIMETTEC 126  
 OY 176 GDVOLLSECAVOSAQMMAVDYPTIVSRNGAGLTIPSPTALSGOYLILTKT-GRPAQT 234  
 DB 127 EPRKHFGCRTRTPPEFNDSTLAGFAYPTDDELGLIMAPARLVGOYRRLAYIDGTVAYT 186  
 OY 235 -ALVTLLEVNDRC--LKIGSQINFLPSKQWTEYOYOTGOGFHL-----YR-----I 277  
 DB 187 DPMWLPAGD-CWFESKIDAAARGYFESACFPAREYE--QNKVLILTYLTOTYPOEAKKAI 242  
 OY 278 AD-INTRHADY-----YRGYEDILORNNLNRKNPSAPDRPDSVPOEIPAVTKKAE 330  
 DB 243 VDYFMFRHGGVPPYFEESKGYE-----PPPAAGD---GSPAPPGDDE 282  
 OY 331 GRTPDASSSEKKAPPEDESDMOAASGENPALPEDEDEVPEDEHDDPSDDYINDMP 390  
 DB 283 AREDEGETEDGAAGREGNGRPPGEGGESPT--PEANGAEGEPKFPSPDADRECGWP 340  
 OY 391 AV-----IYEETTKSSNAVSMPIFAAFVACAVALV 421  
 DB 341 SLEAITHPAPATPPADPAVPGVGIGIAAIAICV 377

RESULT 13  
 GAK\_HUMAN  
 ID VGLX\_PRIV1 STANDARD; PRT; 498 AA.  
 AC P07362;

DT 01-APR-1988 (Rel. 07, Created)  
 DT 01-APR-1988 (Rel. 07, Last sequence update)  
 DT 01-DEC-1992 (Rel. 24, Last annotation update)  
 DE Secreted glycoprotein GX.  
 GN GX.  
 OS Pseudorabies virus (strain Rice) (PRV).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Varicellovirinae.  
 OX NCBI\_TaxID=10350;  
 RN [1]  
 RP MEDLINE=85135070; PubMed=2983115;  
 RX Rea T.J., Timmins J.G., Long G.W., Post L.E.;  
 RT "Mapping and sequence of the gene for the pseudorabies virus  
 glycoprotein which accumulates in the medium of infected cells.";  
 RL J. Virol. 54:21-29(1985).  
 CC -I- SIMILARITY: TO EBV-1 GLYCOPROTEIN G.

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EMBL: M10986; AAC35206.1; -  
 DR PIR: A21879; VGBEGX.  
 DR InterPro: IPR003363; Herpes-gC.  
 DR Pfam: PF02400; Herpes-gC.1.  
 KW Glycoprotein.  
 FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 226 226 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 498 AA; 53721 MW; 17DEA180672A62DD CRC64;

Query Match 5.6%; Score 129; DB 1; Length 498;  
 Best Local Similarity 23.5%; Pred. No. 0.024;  
 Matches 73; Conservative 32; Mismatches 115; Indels 90; Gaps 13;

OY 95 ALDALTPAVGPNRYLTVRSRGCDVVELNPSVNDMTISAKEKEKGPEASVVEYV 154  
 DB 43 ATPAQPYNPLAPANATGTDYSRCCEMLLDPLDVSSRS-----DPVNVTVAMFP- 93  
 OY 155 IKGDGEDKXCPYRKREYREC-GD-----VOLSECAVOSAQMMAVD 195  
 DB 94 ----DGHCCKVPLVHREYIGCCPDAMPSEVETCGYSTRTRIDTLMETALVNASL---- 145  
 OY 196 YVSTLVSRNGAGLTIFSPALSGOYLILTKIGRPAOTALVLEVNDRCIKIGSQLNEL 255  
 DB 146 -----VLQGLYDAGLYIVLVFGDDAYLGTVSVEAN-----L 180  
 OY 256 PSKQWTEQYOTGOGFHLPTADTNTRHADYVYCYEDILORNNLNRKNPSAPDRP 315  
 DB 181 DYPGKKGHLITTRBATIPPIAPTAGDH-----QRWGCCT-----PST 219  
 OY 316 DSVPOEIPAVTKKAEGRPD-AESSEKKAPPEDESDMOAASGENPALPEDEVPDPT 374  
 DB 220 DEGAWE--NVTAAEKGLSDYADYDVHIFRESQDEV---VHGDAFPA-PGEVYTBEE- 272  
 OY 375 EHDHPNSDDP 384  
 DB 273 EAEILTSSDLD 282

RESULT 14  
 GAK\_HUMAN  
 ID O14976; Q9BYV6; STANDARD; PRT; 1311 AA.  
 AC O14976;

DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Cyclin G-associated kinase (EC 2.7.1.1-).  
 GN GAK.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
 RC TISSUE=Fibroblast;  
 RX MEDLINE=97446136; PubMed=9299234;  
 RA Kimura S.H., Tsutsumi H., Yabuta N., Endo Y., Nojima H.;  
 RT "Structure, expression, and chromosomal localization of human GAK.";  
 RL Genomics 44:179-187(1997).  
 RN [2]  
 RP SEQUENCE OF 981-1311 FROM N.A.

CC Strausberg R.;  
 CC Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 CC FUNCTION: AND SUBCELLULAR LOCATION.  
 CC MEDLINE=20092914; PubMed=10625686;  
 CC Greener T., Zhao X., Nojima H., Eisenberg E., Greene L.E.;

RT "Role of cyclin G-associated kinase in uncoating clathrin-coated vesicles from non-neuronal cells";  
 RL J. Biol. Chem. 275:1365-1370(2000);  
 CC -1- FUNCTION: Associates with cyclin G and CDK5. Seems to act as an auxilin homolog that is involved in the uncoating of clathrin-coated vesicles by Hsc70 in non-neuronal cells. Expression oscillates slightly during the cell cycle, peaking at G1.  
 CC -1- SUBCELLULAR LOCATION: Localizes to the perinuclear area and to the trans-Golgi network. Also seen on the plasma membrane, probably at focal adhesions.  
 CC -1- TISSUE SPECIFICITY: Ubiquitous. Highest in testis.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC -1- SIMILARITY: CONTAINS 1 TENSIN DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 J DOMAIN.  
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 CC -----  
 DR EMBL: D88435; BAA22623.1; -  
 DR EMBL: BC000816; AAH00816.1; -  
 DR EMBL: BC008668; AAH08668.1; -  
 DR Genew; HGNC:4113; GAK.  
 DR MIM: 602052; -  
 DR InterPro: IPR001623; DnaJ\_N.  
 DR InterPro: IPR000713; Euk\_Pkinase.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR InterPro: IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR Pfam; PF00226; DnaJ; 1.  
 DR ProDom; PD000001; Euk\_pkinase; 1.  
 DR SMART; SM00271; DnaJ; 1.  
 DR SMART; SM00220; S\_TKC; 1.  
 DR SMART; SM00219; TyrKC; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
 DR PROSITE; PS0011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE; PS00636; DnaJ\_1; FALSE\_NEG.  
 DR PROSITE; PS0076; DnaJ\_2; 1.  
 KW Transferrase: Serine/threonine-protein kinase; ATP-binding;  
 KW Nuclear protein; Endoplasmic reticulum; Cell cycle.  
 FT ACT\_SITE 173 314  
 FT DOMAIN 173 350  
 FT DOMAIN 407 691  
 FT DOMAIN 1247 1311  
 FT CONFLICT 1113 1113 J-DOMAIN.  
 FT SEQUENCE 1311 AA; 143190 MW; 0ACE45DF57A5F981 CRC64;  
 SQ  
 Query Match 5.1%; Score 118.5; DB 1; Length 1311;  
 Best Local Similarity 19.5%; Pred. No. 0.54;  
 Matches 96; Conservative 74; Mismatches 144; Indels 179; Gaps 28;  
 OY 4 PHLRRSHRYAKGEVLNKHMDG--GKRCSGAAVFTLFWTC-----VRIMREHICVR 55  
 DB 457 PRTYRPSRFH-----NRVSECGMAARR--APHLHTLYNCRMMHAWLRDQHNKVCV- 506  
 OY 56 NAMDRHLFLRAFWTIVLLSFASSOSTAAYTYDILGRALDALTIPAVGP-YNRYLRLV 114  
 DB 507 HCMQGRAASAVVCSFLCFPLFSTAEAAV-YMFSMKR-----CPPEIWSHKRYLEYM 559  
 OY 115 SRGCDVVELNPIISVNDMISAKEKEGKGPVAVFVYI-----KDDGEDKXCP 166  
 DB 560 ---CDMAVEEPII-----PHSKPIIVAAVMTPTPLPFSKRSGRPRCE 600  
 OY 167 IY-----RKERYECGDVOLLSECAVOSQAMVADVSTLVSRRAGLITFSPTAA 217  
 DB 601 VYVDERVAVSQTEYDKMRDKIEDKAV-----IDLGTVAGQDVLIVYHARST 650

OY 218 LSGGLYLLTKIGRFAQTALVTVLVNDRLCKIGSGLNPLPSKOWTTE--QYOTGGEGEHLX 275  
 DB 651 LGR-----LQAKMAMKM--FQIOFHTGEVPRNATYVFAKAYDL----- 688  
 OY 276 PIADNTRHADDVRYGVEDILO-----RW>NNLIRKKNP---SAPD 312  
 DB 689 -----DADCIQKRYDLCQVNLVEVEPRDRSREAPPNENSMGLNPKILFSSRE 740  
 OY 313 PRPD-----SVPEIIPAVTKK--AGRPDAESSKKAPDESD-----DMQA 354  
 DB 741 EQQDILSKFGKPELPQ--PGSTAQYDAGAGSFEAPETDSPPSSASASRLHTLDQE 799  
 OY 355 E-----ASGENPALPED-----DE--VPEDTEHDDPKSDPD----- 384  
 DB 800 EKEAETGAENASSKSESALMEDRDESEVSDGGSFISSEGOEPRADEPGLAALVQO 859  
 OY 385 ---YYNDMPAVIP 394  
 DB 860 DLVEFETPAVLIP 872  
 RESULT 15  
 XPR6\_YARLI STANDARD; PRT; 976 AA.  
 AC P42781;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Dipeasic processing endoprotease precursor (EC 3.4.21.-).  
 GN XPR6.  
 OS Yarrowia lipolytica (Candida lipolytica).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 CC Saccharomycetales; Dipodascaceae; Yarrowia.  
 OX NCBI\_TaxID=4952;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CX-161-1B;  
 RX MEDLINE=94262316; PubMed=8203153;  
 RA Enderlin C.S., Ogrzydzik D.M.;  
 RT "Cloning, nucleotide sequence and functions of XPR6, which codes for a dipeasic processing endoprotease from the yeast Yarrowia lipolytica."  
 RT 1 lipolytica."  
 RL Yeast 10:67-79(1994).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8. PURIN SUBFAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: L16238; AAA20573.1; -  
 DR HSSP: Q45670; IDBI.  
 DR MEROPS: S08\_070; -  
 DR InterPro: IPR002884; P\_domain.  
 DR InterPro: IPR000209; Peptidase\_S8.  
 DR Pfam; PF00082; Peptidase\_S8; 1.  
 DR Pfam; PF01483; P; PARTIAL.  
 DR PRINTS; PRO0723; SUBTILISIN.  
 DR ProDom; PD000717; P\_domain; 1.  
 DR PROSITE; PS00136; SUBTILASE\_ASP; 1.  
 DR PROSITE; PS00137; SUBTILASE\_HIS; 1.  
 DR PROSITE; PS00138; SUBTILASE\_SER; 1.  
 KW Hydrolase: Serine protease; Glycoprotein; Calcium; Transmembrane;  
 KW Zymogen; Signal.  
 FT SIGNAL 1 17  
 FT CHAIN 18 976  
 FT DOMAIN 211 230  
 FT TRANSMEM 524 544  
 FT TRANSMEM 855 875  
 FT ACT\_SITE 311 311  
 POTENTIAL.  
 DIABASIC PROCESSING ENDOPEPTIDASE.  
 ASP/GLU-RICH (HIGHLY ACIDIC).  
 POTENTIAL.  
 POTENTIAL.  
 CHARGE RELAY SYSTEM (BY SIMILARITY).

FT ACT\_SITE 349 349 CHARGE RELAY SYSTEM (BY SIMILARITY).  
FT ACT\_SITE 528 528 CHARGE RELAY SYSTEM (BY SIMILARITY).  
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 886 886 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 976 AA: 110024 MW: 038C5999E7E8F6F6 CRC64;

Query Match 5.0%; Score 116; DB 1; Length 976;  
Best Local Similarity 23.9%; Pred. No. 0.56; Indels 40; Gaps 8;

Matches 57; Conservative 31; Mismatches 110; Indels 40; Gaps 8;

QY 216 AALSGOYLLTKIGRFQATVLTLEVNDRCLKIGSQLNPLPSKWCWTQYQTGFGGHELY 275  
DB 657 ASYRGHVRLKGRGVVSELAALRRDRSKDGYNNAFMSVAHWADE-----GGGDW 709  
QY 276 PIADINTNHAD-----DYYRGYEDILQRMNNLLRKKNPSPADPRDSVPQEIIPAVT 326  
DB 710 ELTVENTGEODQVELVNMQLNVFGEQKD--KREENKEGESKPEDENKKEGEKKEKPEDE 767  
QY 327 KKAEGRTPDASSEKKAPPEDESDMQAASGENPALPED--DEVPEDTEHDPNSDPD 384  
DB 768 NKEGKNKEDDKGDKEDKPEDEKPEDE-----KPEDTPEDKPEDEKPEDEKPEDEK 818  
QY 385 YNDMPAVIPEVETTKSSNAVSMPIF-----AAFVACAVALVG--LLVWSIVKC 431  
DB 819 KPEEKPEEKPYDNDSSSDSSDSSHTSWMPDLSSKSAWLGVALLVGFTAVIGIYAC 876

Search completed: February 19, 2003, 16:21:35  
Job time : 16 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 19, 2003, 16:21:11 ; Search time 35 Seconds  
(without alignments)  
2554.984 Million cell updates/sec

Title: US-09-994-064-11

Perfect score: 2311  
Sequence: 1 MHRPHLRHSRYAKGEVLN.....ACAVLVGLLWSIVKARS 434

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: SP archaea: \*  
2: SP bacteria: \*  
3: SP fungi: \*  
4: SP human: \*  
5: SP invertebrate: \*  
6: SP mammal: \*  
7: SP mhc: \*  
8: SP organelle: \*  
9: SP phage: \*  
10: SP plant: \*  
11: SP rodent: \*  
12: SP virus: \*  
13: SP vertebrate: \*  
14: SP unclassified: \*  
15: SP virus: \*  
16: SP bacteriophage: \*  
17: SP archaea: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2311	100.0	434	12	067644 gallid herp
2	1860	80.5	371	12	069294 gallid herp
3	190	8.2	394	12	069082 human herpe
4	190	8.2	394	12	069081 human herpe
5	190	8.2	394	12	005059 human herpe
6	190	8.2	394	12	005060 human herpe
7	188	8.1	394	12	080RB6 human herpe
8	186.5	8.1	394	12	0991M3 human herpe
9	184	8.0	394	12	091NH6 human herpe
10	180	7.8	394	12	08GRB7 human herpe
11	175	7.6	402	12	004245 equine herp
12	169	7.3	400	12	091W02 pseudorabie
13	169	7.3	516	12	091W00 pseudorabie
14	162.5	7.0	374	12	089634 feline herp
15	162	7.0	398	12	09YS31 pseudorabie
16	159	6.9	404	12	092290 pseudorabie

17	159	6.9	417	12	065535 bovine herp
18	158	6.8	393	12	069467 herpes simp
19	151.5	6.6	403	12	067648 turkey herp
20	151.5	6.6	403	12	0966L6 turkey herp
21	146	6.3	402	12	039308 equine herp
22	146	6.3	402	12	086652 equine herp
23	141.5	6.1	403	12	069286 turkey herp
24	135.5	5.9	395	12	069369 cercopithe
25	134	5.8	385	12	09E939 gallid herp
26	134	5.7	385	12	012378 marek's dis
27	131.5	5.7	384	12	09DP33 turkey herp
28	131.5	5.7	384	12	088523 turkey herp
29	129	5.6	489	12	0913H9 pseudorabie
30	125	5.4	345	12	041524 canine herp
31	124.5	5.4	394	12	08V2D6 simlan herp
32	124.5	5.4	394	12	08V2D5 simlan herp
33	124.5	5.4	394	12	08UYJ1 simlan herp
34	124.5	5.4	394	12	08UYA3 simlan herp
35	124.5	5.4	394	12	08UYA2 simlan herp
36	123.5	5.3	237	12	041201 pseudorabie
37	122.5	5.3	394	12	08V2D4 simlan herp
38	121.5	5.3	394	12	08UYF8 simlan herp
39	120	5.2	394	12	08V2D3 simlan herp
40	117	5.1	303	10	09M4U5 zea mays (m
41	115.5	5.0	614	5	094674 plasmidium
42	115	5.0	394	12	08V724 simlan herp
43	115	5.0	1648	11	09Q205 mus musculu
44	114	4.9	1370	11	09ESB8 mus musculu
45	114	4.9	1570	11	09ESB6 mus musculu

#### ALIGNMENTS

RESULT 1  
067644 PRELIMINARY: PRT: 434 AA.  
ID 067644  
AC 067644;  
DT 01-NOV-1996 (TREMURel. 01, Created)  
DT 01-NOV-1996 (TREMURel. 01, Last sequence update)  
DT 01-JUN-2001 (TREMURel. 17, Last annotation update)  
DE Glycoprotein D.  
OS Gallid herpesvirus 1.  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae.  
OC Alphaherpesvirinae; Infectious laryngotracheitis-like viruses.  
OX NCBI\_TaxID=10386;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=USDA CHALLENGE STRAIN;  
RX MEDLINE=97033380; PubMed=8879127;  
RA Wild M.A., Cook S., Cochran M.;  
RT "A genomic map of infectious laryngotracheitis virus and the sequence  
RT and organization of genes present in the unique short and flanking  
RT regions";  
RL Virus Genes 12:107-116(1996).  
DR EMBL: U28832; AAC5100.1; -;  
DR InterPro: IPR002896; Herpes\_glycop.D.  
DR Pfam: PF01537; Herpes\_glycop.D: 1.  
SQ SEQUENCE 434 AA: 48472 MW: 7923452625F52 CRC64:  
Query Match 100.0%; Score 2311; DB 12; Length 434;  
Best Local Similarity 100.0%; Pred. No. 6.1e-185;  
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MHRPHLRHSRYAKGEVLNKHMDCCGCCGAAYTLFWTCVIRIREHICFRNAMD 60  
Db 1 MHRPHLRHSRYAKGEVLNKHMDCCGCCGAAYTLFWTCVIRIREHICFRNAMD 60  
QY 61 HLEFLNAFWTIVLLSFAASSTAAYTYDILGRALDALTPAVGPYRRLTRVSRCDV 120  
Db 61 HLEFLNAFWTIVLLSFAASSTAAYTYDILGRALDALTPAVGPYRRLTRVSRCDV 120  
QY 121 VELNPISNVDDMTISAKKEKGGPFASVYWFYIKGDGCEDKCPIYRKREYRCGCVOL 180

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Db 121 VELNLSNVDDMISAKKEKGPPEASVWFYIKGGDEGDKCPITRKREYREGGVQL 180
QY 181 LSECAVQSAQMAWADVSTVLSRNGAGLTTFSPALSGOYLTLTKIGRPAQALVLE 240
Db 181 LSECAVQSAQMAWADVSTVLSRNGAGLTTFSPALSGOYLTLTKIGRPAQALVLE 240
QY 241 VNRCLKIGSOLNLFPSKCTTEYOYOTGFOGHEHLYPIADTNRHADVYRGEDTLQRMN 300
Db 241 VNRCLKIGSOLNLFPSKCTTEYOYOTGFOGHEHLYPIADTNRHADVYRGEDTLQRMN 300
QY 301 NLKKKNSAPDPRDPSVPOEIPAVTKKAGRTDPAESSEKKAPDESEDMDQAEASGEN 360
Db 301 NLKKKNSAPDPRDPSVPOEIPAVTKKAGRTDPAESSEKKAPDESEDMDQAEASGEN 360
QY 361 PALPEDEVEDTEHDDPNSDPDYNDMPAVIPEETTTSSNAVSPITPAFVACAVL 420
Db 361 PALPEDEVEDTEHDDPNSDPDYNDMPAVIPEETTTSSNAVSPITPAFVACAVL 420
QY 421 VGLLWMSIVKCAR 434
Db 421 VGLLWMSIVKCAR 434

```

## RESULT 2

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ID 069294 PRELIMINARY; PRT; 371 AA.
AC 069294;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE glycoprotein D.
GN GD.
OS Gallid herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Infectious laryngotracheitis-like viruses.
OX NCBI_TaxID=10386;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SA-2;
RX MEDLINE=95337426; PubMed=7612933;
RA Johnson M.A., Tyack S.G., Pridaux C.T., Kongsuwan K., Sheppard M.;
RT "Sequence characteristics of a gene in infectious laryngotracheitis
RT virus homologous to glycoprotein D of herpes simplex virus. ";
DR EMBL: L31965; AAA88925.1;
DR InterPro: IPR002896; Herpes_glycop_D.
DR Pfam: PF01537; Herpes_glycop_D.1.
SQ SEQUENCE 371 AA; 41229 MW; AE81A493112A4489 CRC64;

```

## Query Match

Best Local Similarity 80.5%; Score 1860; DB 12; Length 371;

Matches 355; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

```

QY 58 MDRHLFLRNAFTIYLSSFSASQSTAAYDYLLGRALDALTIYAVGPNRYLTVRSNG 117
Db 1 MDRHLFLRNAFTIYLSSFSASQSTAAYDYLLGRALDALTIYAVGPNRYLTVRSNG 60
QY 118 CDVLELNPISNDDMISAKEKEKGPPEASVWFYIKGGDEGDKCPITRKREYREGCD 177
Db 61 CDVLELNPISNDDMISAKEKEKGPPEASVWFYIKGGDEGDKCPITRKREYREGCD 120
QY 178 VOLLSECAVQSAQMAWADVSTVLSRNGAGLTTFSPALSGOYLTLTKIGRPAQALV 237
Db 121 VOLLSECAVQSAQMAWADVSTVLSRNGAGLTTFSPALSGOYLTLTKIGRPAQALV 180
QY 238 TLEVNDRLKIGSOLNLFPSKCTTEYOYOTGFOGHEHLYPIADTNRHADVYRGEDTLQ 297
Db 181 TLEVNDRLKIGSOLNLFPSKCTTEYOYOTGFOGHEHLYPIADTNRHADVYRGEDTLQ 240
QY 298 RWNLLRKKNSAPDPRDPSVPOEIPAVTKKAGRTDPAESSEKKAPDESEDMDQAEAS 357
Db 241 RWNLLRKKNSAPDPRDPSVPOEIPAVTKKAGRTDPAESSEKKAPDESEDMDQAEAS 300

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QY 358 GENPALPEDEVEDTEHDDPNSDPDYNDMPAVIPEETTTSSNAVSPITPAFVACA 417
Db 301 GENPALPEDEVEDTEHDDPNSDPDYNDMPAVIPEETTTSSNAVSPITPAFVACA 360
QY 418 VALVG 422
Db 361 VALVG 365

```

## RESULT 3

```

ID 069082 PRELIMINARY; PRT; 394 AA.
AC 069082;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE glycoprotein D precursor.
OS human herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10298;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94160582; PubMed=8116256;
RA Dean H.J., Terhune S.S., Shieh M.T., Spear P.G.;
RT "Single amino acid substitutions in glycoprotein D of herpes simplex
RT virus type 1 that confer resistance to gd-mediated interference also
RT alter virus infectivity. ";
RL Virology 199:67-80(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Dean H.J., Terhune S.S., Johnson R.M., Spear P.G.;
RT "Variability among strains of Herpes simplex virus in sensitivity to
RT gd-mediated interference. ";
RL Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL: L09244; AAA19631.1;
DR InterPro: IPR002896; Herpes_glycop_D.
DR InterPro: IPR001400; Somatotropin.
DR Pfam: PF01537; Herpes_glycop_D.1.
DR PROSITE: PS00266; SOMATOTROPIN_1; UNKNOWN_1.
KM Signal.
FT SIGNAL 1 25
FT CHAIN 26 394 GLYCOPROTEIN D.
FT VARIANT 52 52 R->Q (IN REF. 2).
SQ SEQUENCE 394 AA; 43344 MW; 1076f2f0c8a1d73e CRC64;

```

## Query Match

Best Local Similarity 8.2%; Score 190; DB 12; Length 394;

Matches 78; Conservative 47; Mismatches 145; Indels 66; Gaps 14;

```

QY 106 PYNRRLTVRSNGCDVLELNPISNDDMISAKEKEKGPPEASVWFYIKGGDEGDKYC 165
Db 79 PYTYAVVLEKACSVLNLNAPSSEAPQIVRGASEVRRQPYLTLTAMPRM-----GGCAIC 133
QY 166 PIYKREYREGCDVOLLSECAVQSAQMAWADVPS-TVLSRNGAGLTTFSPALSGOYL 224
Db 134 PIYWEYTECSYNSLIGCPITQPRW--NYDSFSAVSEDNGLFLHNAFAETAGTYLR 191
QY 225 TLTKIGRPAQALVLE--VNRCLKIGSOLNLFPSKCTTEYOYOTG-----FOG 271
Db 192 LVKINDMTEITQFLEHRAKGC-KYALPLRTPSACLSQAQOQGYTVDSIGMLPRFIP 250
QY 272 EHLPIADTNRHADVYRGEDTLQRMNLLRKKNSAPDPRDPSVPOEIPAVTKKAG 331
Db 251 ENQRTAVVYSLIKG-----WH-----GKAP-YSTLTPRL-----S 293
QY 332 RTPAESSEKKAPDESEDMDQAEASGENPALPEDEVEDTEHDDPNSDPDYNDMP 390
Db 284 ETPNA--TOELAPDEDEDSALLIEDRYGAQIPRMWHITPSQDADATRYHPRATPRNMG 341
QY 391 AVIPVEETTTSSNAVSPITPAFVACAVLVLW 426

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Db 342 LI-----AGAVGSLAALVYC-----GIYWM 363

## RESULT 4

Q69081 PRELIMINARY; PRT; 394 AA.

AC Q69081;  
DT 01-NOV-1996 (Tremblrel. 01, Created)  
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE Glycoprotein D precursor.  
OS human herpesvirus 1.  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Alphaherpesvirinae; Simplexvirus.  
NCBI\_TaxId=10298;

RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94160582; Pubmed=8116256;  
RA Dean H.J., Terhune S.S., Shieh M.T., Spear P.G.;  
RT "Single amino acid substitutions in glycoprotein D of herpes simplex virus type 1 that confer resistance to gp-mediated interference also alter virus infectivity."  
RT Virology 199;67:80(1994).  
RL [2]  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Dean H.J., Terhune S.S., Johnson R.M., Spear P.G.;  
RT "Variability among strains of Herpes simplex virus in sensitivity to gp-mediated interference."  
RT Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.  
RL EMBL; L09245; AAA19630.1; .  
DR InterPro: IPR002896; Herpes\_glycop\_D.  
DR InterPro: IPR001400; Somatotropin.  
DR Pfam: PF01537; Herpes\_glycop\_D; 1.  
DR PROSITE: PS00266; SOMATOTROPIN\_1; UNKNOWN\_1.  
KW Signal.  
FT SIGNAL 1 25 POTENTIAL.  
FT CHAIN 26 394 GLYCOPROTEIN D.  
FT VARIANT 52 52 P -> Q (IN REF. 1 AND 2).  
SQ SEQUENCE 394 AA; 43285 MW; 7FBE5BA1E8FDC0BF CRC64;

Query Match 8.2%; Score 190; DB 12; Length 394;  
Best Local Similarity 23.2%; Pred. No. 1.3e-07;

Matches 78; Conservative 47; Mismatches 145; Indels 66; Gaps 14;

QY 106 PYNRYLTRVSGCDVVELNPISNVDMISAKEKEKGPPEASVYVYIKGDDGEKVC 165  
DB 79 PITYVYAVLERACRSVLLNPSEAPQIVRGASEDVRKQPYNLITAMFRM-----GNCAL 133  
QY 166 PIYKEVREGCDVOLLSECAVOSQOMWADVPS-TLVSRNGAGLTIESPTAALSGQYL 224  
DB 134 PITYMETECSYKNSLACPIRTOPRW--NYDSFSAVSEDNIGFLMHARAFETAGTYLR 191  
QY 225 TLKIGRPAQTALVLE--VNDRCIKIGSOLNPLPSKCTTEQYOTG-----FOG 271  
DB 192 LVKINDTEITQFLIHRAGSC-KYALPLRIPSACTSPQAVYQGVTVDSIGMLPRFIP 250  
QY 272 EHLPIADTTRHADVDYRGYEDILQRMNMLRKKNPSADPRDSVPOEIPAVTKAEG 331  
DB 251 ENORTAVVISIKTAG-----WH-----GKAP-VYSTLLPPEL-----S 283  
QY 332 RTPDAESSEKAPPEDESD-MQAEASGENPALPEDEVEDTEHDDPSDDPYNDMP 390  
DB 284 ETRNA--TOPELAPDEDESDALLEDEYGVTAPOQIPRMWHIPSIQDATTYHNPATPRNMG 341  
QY 391 AVIPVEETTKSSNAVSPITFAAFYACAVALLGLIWM 426  
DB 342 LI-----AGAVGSLAALVYC-----GIYWM 363

RESULT 5  
Q05059 PRELIMINARY; PRT; 394 AA.  
ID Q05059  
AC Q05059;

DT 01-NOV-1996 (Tremblrel. 01, Created)  
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
DE Glycoprotein D precursor.  
OS human herpesvirus 1.  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Alphaherpesvirinae; Simplexvirus.  
NCBI\_TaxId=10298;

RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-E;  
RX MEDLINE=94160582; Pubmed=8116256;  
RA Dean H.J., Terhune S.S., Shieh M.T., Spear P.G.;  
RT "Single amino acid substitutions in gp of herpes simplex virus 1 confer resistance to gp-mediated interference and cause cell-type-dependent alterations in infectivity."  
RT Virology 199;67:80(1994).  
RL [1]  
CC -1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1: GH, GB, GC, GG, GD, GI, AND GE.  
CC -1- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEIN D.  
DR EMBL; L09242; AAB59754.1; .  
DR InterPro: IPR002896; Herpes\_glycop\_D.  
DR InterPro: IPR001400; Somatotropin.  
DR Pfam: PF01537; Herpes\_glycop\_D; 1.  
DR PROSITE: PS00266; SOMATOTROPIN\_1; UNKNOWN\_1.  
KW Glycoprotein; Transmembrane; Signal.  
FT SIGNAL 1 25 POTENTIAL.  
FT CHAIN 26 394 GLYCOPROTEIN D.  
FT DOMAIN 26 339 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 340 364 POTENTIAL.  
FT DOMAIN 365 381 STRONGLY BASIC REGION; WHICH PROBABLY SERVES TO ANCHOR THE GLYCOPROTEIN IN THE MEMBRANE.  
FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 394 AA; 43307 MW; 90593F3C19486AC5 CRC64;

Query Match 8.2%; Score 190; DB 12; Length 394;  
Best Local Similarity 23.2%; Pred. No. 1.3e-07;

Matches 78; Conservative 47; Mismatches 145; Indels 66; Gaps 14;

QY 106 PYNRYLTRVSGCDVVELNPISNVDMISAKEKEKGPPEASVYVYIKGDDGEKVC 165  
DB 79 PITYVYAVLERACRSVLLNPSEAPQIVRGASEDVRKQPYNLITAMFRM-----GNCAL 133  
QY 166 PIYKEVREGCDVOLLSECAVOSQOMWADVPS-TLVSRNGAGLTIESPTAALSGQYL 224  
DB 134 PITYMETECSYKNSLACPIRTOPRW--NYDSFSAVSEDNIGFLMHARAFETAGTYLR 191  
QY 225 TLKIGRPAQTALVLE--VNDRCIKIGSOLNPLPSKCTTEQYOTG-----FOG 271  
DB 192 LVKINDTEITQFLIHRAGSC-KYALPLRIPSACTSPQAVYQGVTVDSIGMLPRFIP 250  
QY 272 EHLPIADTTRHADVDYRGYEDILQRMNMLRKKNPSADPRDSVPOEIPAVTKAEG 331  
DB 251 ENORTAVVISIKTAG-----WH-----GKAP-VYSTLLPPEL-----S 283  
QY 332 RTPDAESSEKAPPEDESD-MQAEASGENPALPEDEVEDTEHDDPSDDPYNDMP 390  
DB 284 ETRNA--TOPELAPDEDESDALLEDEYGVTAPOQIPRMWHIPSIQDATTYHNPATPRNMG 341  
QY 391 AVIPVEETTKSSNAVSPITFAAFYACAVALLGLIWM 426  
DB 342 LI-----AGAVGSLAALVYC-----GIYWM 363

RESULT 6  
Q05060 PRELIMINARY; PRT; 394 AA.  
ID Q05060  
AC Q05060;  
DT 01-NOV-1996 (Tremblrel. 01, Created)  
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)

01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 Glycoprotein D precursor.  
 human herpesvirus 1.  
 Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 Alphaherpesvirinae; Simplexvirus.  
 NCBI\_TaxID=10298;  
 [1]  
 SEQUENCE FROM N.A.  
 MEDLINE=94160582; PubMed=8116256;  
 Dean H.J., Terhune S.S., Shieh M.T., Spear P.G.;  
 "Single amino acid substitutions in gp of herpes simplex virus 1  
 confer resistance to gp-mediated interference and cause cell-type-  
 dependent alterations in infectivity."  
 Virology 199;67-80(1994).  
 -1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV-1: GH,  
 GB, GC, GG, GD, GI, AND GE.  
 -1- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEIN D.  
 EMBL: L09243; AAA19629.1; -  
 InterPro: IPR002896; Herpes-glycop.D.  
 Pfam: PF01537; Herpes-glycop.D; 1.  
 PROSITE: PS00266; SOMATOTROPIN\_1; UNKNOWN\_1.  
 Glycoprotein; Transmembrane; Signal.  
 SIGNAL 1 25  
 CHAIN 26 394  
 DOMAIN 26 339  
 TRANSMEM 340 364  
 DOMAIN 365 381  
 POTENTIAL.  
 GLYCOPROTEIN D.  
 EXTRACELLULAR (POTENTIAL).  
 POTENTIAL.  
 STRONGLY BASIC REGION;  
 WHICH PROBABLY SERVES TO ANCHOR THE  
 GLYCOPROTEIN IN THE MEMBRANE.  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CARBOHYD 119 119  
 CARBOHYD 146 146  
 CARBOHYD 287 287  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SEQUENCE 394 AA; 43316 MW; 90540F0F1953CB7F CRC64;  
 Query Match 8.2%; Score 190; DB 12; Length 394;  
 Best Local Similarity 23.2%; Pred. No. 1.3e-07;  
 Matches 78; Conservative 47; Mismatches 145; Indels 66; Gaps 14;  
 Db 106 PYNRYLTVSRGCDVVELNPISVNDMISAAREKEGGEPEASVWFYIKGDDGDEKXC 165  
 79 PIIVYVAVERACRSVLLNAPSEAPQIVRGASEDVKKOPYNLTIAFRM-----GNCNAI 133  
 QY 166 PIYKREYREGCDVOLLSECAVOSQMMADVPS-TLVSRNGAGLTIFSPALSGOYLL 224  
 134 PIYMEYTECSYKSLGACPIRTQPRW--NYDSFSAVSEDNLGFLMHPAFETAGTYLR 191  
 QY 225 TLKIGRFQATLVLE--VNDRCIKIGSOLNLPSCKWTTEYOYQG-----FOG 271  
 192 LVKINDWTEITQFLEHRAKSGC-KYALPLRIPPSACLSPOAVQGVTVDSIGMLPRFTIP 250  
 Db 272 EHLPIADNTFRHADVYGYEDILQRMNNLKKKNSAPDRPDSVQOEIPAVTKKAG 331  
 251 ENQRTVAAYSLKTAG-----WH-----GPKAP-YTSTLLPEL-----S 283  
 QY 332 RPPDAESSKKAPPEDESD-MQAEASGENPALPEDEDETHDNDSPDYNDMP 390  
 284 ETPNA--TQPELAPDEPDESALLEDPVGTVAQIIPNNHIFSIQDAAPFYHPAPATPNMG 341  
 QY 391 AVIPEETTKSSNAVSMPIFAFVACAVALLGLTW 426  
 Db 342 LI-----AGAVGSLTALALVIC-----GIYVW 363  
 RESULT 7  
 Q080R6 PRELIMINARY; PRT; 394 AA.  
 Q080R6;  
 01-JUN-2002 (Tremblrel. 21, Created)  
 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 Glycoprotein D.  
 human herpesvirus 1.

Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 Alphaherpesvirinae; Simplexvirus.  
 NCBI\_TaxID=10298;  
 [1]  
 SEQUENCE FROM N.A.  
 RC STRAIN=KHS2;  
 RA Kim J.K., Kim Y.K., Hong J.B., Kim S.Y., Ahn J.K.;  
 "Isolation of the enhanced neurovirulent HSV-1 strains from Korean  
 patients."  
 Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 EMBL: AF487902; AAL90884.1; -  
 DR EMBL: AF487902; AAL90884.1; -  
 SEQUENCE 394 AA; 43286 MW; 8750DAC984CDS25D CRC64;  
 Query Match 8.1%; Score 188; DB 12; Length 394;  
 Best Local Similarity 23.2%; Pred. No. 1.8e-07;  
 Matches 78; Conservative 47; Mismatches 145; Indels 66; Gaps 14;  
 Db 106 PYNRYLTVSRGCDVVELNPISVNDMISAAREKEGGEPEASVWFYIKGDDGDEKXC 165  
 79 PIIVYVAVERACRSVLLNAPSEAPQIVRGASEDVKKOPYNLTIAFRM-----GNCNAI 133  
 QY 166 PIYKREYREGCDVOLLSECAVOSQMMADVPS-TLVSRNGAGLTIFSPALSGOYLL 224  
 134 PIYMEYTECSYKSLGACPIRTQPRW--NYDSFSAVSEDNLGFLMHPAFETAGTYLR 191  
 QY 225 TLKIGRFQATLVLE--VNDRCIKIGSOLNLPSCKWTTEYOYQG-----FOG 271  
 192 LVKINDWTEITQFLEHRAKSGC-KYALPLRIPPSACLSPOAVQGVTVDSIGMLPRFTIP 250  
 Db 272 EHLPIADNTFRHADVYGYEDILQRMNNLKKKNSAPDRPDSVQOEIPAVTKKAG 331  
 251 ENQRTVAAYSLKTAG-----WH-----GPKAP-YTSTLLPEL-----S 283  
 QY 332 RPPDAESSKKAPPEDESD-MQAEASGENPALPEDEDETHDNDSPDYNDMP 390  
 284 ETPNA--TQPELAPDEPDESALLEDPVGTVAQIIPNNHIFSIQDAAPFYHPAPATPNMG 341  
 QY 391 AVIPEETTKSSNAVSMPIFAFVACAVALLGLTW 426  
 Db 342 LI-----AGAVGSLTALALVIC-----GIYVW 363  
 RESULT 8  
 Q091M3 PRELIMINARY; PRT; 394 AA.  
 Q091M3;  
 01-JUN-2001 (Tremblrel. 17, Created)  
 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
 01-OCT-2001 (Tremblrel. 18, Last annotation update)  
 Glycoprotein D.  
 human herpesvirus 1.  
 Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 Alphaherpesvirinae; Simplexvirus.  
 NCBI\_TaxID=10298;  
 [1]  
 SEQUENCE FROM N.A.  
 RA Xiaojuan L., Mingzhao Z.;  
 Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 EMBL: AF333383; AAK19597.1; -  
 DR EMBL: AF333383; AAK19597.1; -  
 DR InterPro: IPR002896; Herpes-glycop.D.  
 DR InterPro: IPR001400; Somatotropin.  
 Pfam: PF01537; Herpes-glycop.D; 1.  
 PROSITE: PS00266; SOMATOTROPIN\_1; UNKNOWN\_1.  
 SEQUENCE 394 AA; 43277 MW; E7294F3C19486AC0 CRC64;  
 Query Match 8.1%; Score 186.5; DB 12; Length 394;  
 Best Local Similarity 23.2%; Pred. No. 2.5e-07;  
 Matches 76; Conservative 46; Mismatches 145; Indels 61; Gaps 13;  
 Db 106 PYNRYLTVSRGCDVVELNPISVNDMISAAREKEGGEPEASVWFYIKGDDGDEKXC 165  
 79 PIIVYVAVERACRSVLLNAPSEAPQIVRGASEDVKKOPYNLTIAFRM-----GNCNAI 133

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OY 166 PIYKREYRECGDVQLLSECAVSAQMAVAVYPS--TIVSRNGAGLTIFSPALSGOYL 224
  || || || || || || || || || || || || || || || || || || || || ||
DB 134 PTWMEYRECSYKNSLGCAPITQPRW--NYDSESAVSEDMGLMHAFAETAGTYLR 191
OY 225 TLKIGRFAQTALVLE--VNDRCCLKIGSOLNPLPSKCWTTEOYOTG-----FOG 271
  || || || || || || || || || || || || || || || || || || || || ||
DB 192 LVKINDMEITQFILEHRAKGCSC-KYALPLRIPFACLSPOAYQGVVDSIGMLPRFIP 250
OY 272 EHLVFIADTNRHADVDYRGYEDILQRRNNLLRKKNPSPAPRPSPOEIPAVTKKAE 331
  || || || || || || || || || || || || || || || || || || || || ||
DB 251 ENQRTVAVYSLKTAG-----WH-----GPKAP-YTSTLLPEL-----S 283
OY 332 RPPDAESSEKKAPRDESD--MQAEASGENPALPEDEVEDTEHDDPNSDPDYNDMP 390
  || || || || || || || || || || || || || || || || || || || || ||
DB 284 ETPNA--TQPELAPRDEPDSALLEDPVGTAVAPQIRPMNHITSIDAAITPHPPATPNMG 341
OY 391 AVIPEETTKSSNAVSMPIFAFVACAV 418
DB 342 LI-----AGAVGSLALALVYICGI 360

RESULT 9
O91NH6 PRELIMINARY; PRT; 394 AA.
AC O91NH6:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Glycoprotein D.
GN GD.
OS human herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10298;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=;
RA Lee H.H.;
RT "Cloning, sequencing and baculovirus-based expression of the
RT glycoprotein D gene of Herpes simplex virus type 1 strain F.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF293614; AAK93950.1;
DR InterPro: IPR002896; Herpes_glycop_D.
DR InterPro: IPR001400; Somatotropin.
DR Pfam: PF01537; Herpes_glycop_D.1.
DR PROSITE: PS00266; SOMATOTROPIN_1; UNKNOWN_1.
SQ SEQUENCE 394 AA; 43344 MW; 541E6C1F9A6CE8 CRC64;

Query Match 8.0%; Score 184; DB 12; Length 394;
Best Local Similarity 24.1%; Pred. No. 4e-07;
Matches 82; Conservative 43; Mismatches 141; Indels 74; Gaps 16;
OY 106 PYNRLTVRSRGCDVVELNPISNVDDMISAKEKKGPFESAVYFVYIKGDGEDKCYC 165
  || || || || || || || || || || || || || || || || || || || || ||
DB 79 PTYYVAVLERACRSVLLNAPSEAPQIVRGASEDVRKQPNULTIMFRM-----GCNCAI 133
OY 166 PIYKREYRECGDVQLLSECAVSAQMAVAVYPS--TIVSRNGAGLTIFSPALSGOYL 224
  || || || || || || || || || || || || || || || || || || || || ||
DB 134 PTWMEYRECSYKNSLGCAPITQPRW--NYDSESAVSEDMGLMHAFAETAGTYLR 191
OY 225 TLKIGRFAQTALVLE--VNDRCCLKIGSOLNPLPSKCWTTEOYOTG-----FOG 271
  || || || || || || || || || || || || || || || || || || || || ||
DB 192 LVKINDMEITQFILEHRAKGCSC-KYALPLRIPFACLSPOAYQGVVDSIGMLPRFIP 250
OY 272 EHLVFIADTNRHADVDYRGYEDILQRRNNLLRKKNPSPAPRPSPOEIPAVTKKAE 331
  || || || || || || || || || || || || || || || || || || || || ||
DB 251 ENQRTVAVYSLKTAG-----WH-----GPKAP-YTSTLLPEL-----S 283
OY 332 RPPDAESSEKKAP--PDS-----EDMQAEASGENPALPEDEVEDTEHDDPNSDPDY 386
  || || || || || || || || || || || || || || || || || || || || ||
DB 284 ETPNAQPE-LAPEAPRDESDALLEDPV-----GTAVAPQIRPMNHITSIDAAITPHPPATP 337
OY 387 NDMPAVIPEETTKSSNAVSMPIFAFVACAVALVGLW 426

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DB 338 NNMGLI-----AGAVGSLALALVYIC-----GIYVW 363

RESULT 10
O80RB7 PRELIMINARY; PRT; 394 AA.
AC O80RB7:
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Glycoprotein D.
OS human herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10298;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KHS1;
RA Kim J.K., Kim Y.K., Hong J.B., Kim S.Y., Ahn J.K.;
RT "Isolation of the enhanced neurovirulent HSV-1 strains from Korean
RT patients.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF487901; AAL90883.1;
SQ SEQUENCE 394 AA; 43240 MW; 725F6AC26B6848FC CRC64;

Query Match 7.8%; Score 180; DB 12; Length 394;
Best Local Similarity 22.9%; Pred. No. 8.6e-07;
Matches 77; Conservative 47; Mismatches 146; Indels 66; Gaps 14;
OY 106 PYNRLTVRSRGCDVVELNPISNVDDMISAKEKKGPFESAVYFVYIKGDGEDKCYC 165
  || || || || || || || || || || || || || || || || || || || || ||
DB 79 PTYYVAVLERACRSVLLNAPSEAPQIVRGASEDVRKQPNULTIMFRM-----GCNCAI 133
OY 166 PIYKREYRECGDVQLLSECAVSAQMAVAVYPS--TIVSRNGAGLTIFSPALSGOYL 224
  || || || || || || || || || || || || || || || || || || || || ||
DB 134 PTWMEYRECSYKNSLGCAPITQPRW--NYDSESAVSEDMGLMHAFAETAGTYLR 191
OY 225 TLKIGRFAQTALVLE--VNDRCCLKIGSOLNPLPSKCWTTEOYOTG-----FOG 271
  || || || || || || || || || || || || || || || || || || || || ||
DB 192 LVKINDMEITQFILEHRAKGCSC-KYALPLRIPFACLSPOAYQGVVDSIGMLPRFIP 250
OY 272 EHLVFIADTNRHADVDYRGYEDILQRRNNLLRKKNPSPAPRPSPOEIPAVTKKAE 331
  || || || || || || || || || || || || || || || || || || || || ||
DB 251 ENQRTVAVYSLKTAG-----WH-----GPKAP-YTSTLLPEL-----S 283
OY 332 RPPDAESSEKKAPRDESD--MQAEASGENPALPEDEVEDTEHDDPNSDPDYNDMP 390
  || || || || || || || || || || || || || || || || || || || || ||
DB 284 ETPNA--TQPELAPRDEPDSALLEDPVGTAVAPQIRPMNHITSIDAAITPHPPATPNMG 341
OY 391 AVIPEETTKSSNAVSMPIFAFVACAVALVGLW 426
DB 342 LI-----AGAVGSLALALVYIC-----GIYVW 363

RESULT 11
O04245 PRELIMINARY; PRT; 402 AA.
AC O04245:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Glycoprotein D precursor.
OS Equine herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=10326;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=92180313;
RA Whalley J.M., Robertson G., Bell C.W., Love D., Elphinstone M.,
RA Wiley L., Craven D.;
RT "Identification and comparative sequence analysis of a gene in equine

```

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DR Pfam: PF01537; Herpes_glycop_D, 1.
DR PRINTS: PR01217; PRICHEXTENSN.
SQ SEQUENCE 400 AA; 44338 MW; E5D3EF94976F1C7E CRC64;

Query Match
Best Local Similarity 21.2%; Score 169; DB 12; Length 400;
Matches 90; Conservative 54; Mismatches 152; Indels 128; Gaps 20;

QY 73 LLSFSAQSSTAAYTYDIILG-----RRALDALTIPAVGPNRYLTR-VSRG 117
D 6 LLAALVARTLLGADVAVAPAPFPPEPAAYPTESWQLTFTVSPSPVGGADVYHTRPLEDP 65
QY 118 CDVEELNPISNVDMISAKEKEGGEPFASVYWFYIKGDGDEKQCP--TYREYREC 175
D 66 CGVVALISDPQVRLNEAVAHNR-PTYRAHVAMTRIADG-----CAHLLEYEVADC 117
QY 176 GDVQLLSECAVQSAQNM---AVDYVPSTLVSRNAGLTIFFSEPTAALSGQY--LTLIKIGR 230
D 118 DPFQIGRCRRRTTPMMWTFPSADYMPF---EDELGLLMVAPGRNNEGQYRLYSVDGVN 174
QY 231 FAPTLAVTLEVNDRC--LAIQSOLFPLSKCTTQOYOTGEOGELHYPIADTNTRHADV 288
D 175 ILTFDEVALPEGGECFPAVDQHRKTKGACAMNDESFRRGV-----DY 217
QY 289 YR-----GVEDILGRNNLLLRKN-----PSA-----PDPRP 315
D 218 MRLLTFEYQOPRPREVNVW---YRKNGRTLPRAVYAAATPYALDPAFPSGSPRRPRP 273
QY 316 DSVQEIIPA-VTKKAEGRTPDAESSEKKAAPDESEDMAQASGEMPAALPEDDEVEDT 374
D 274 RPRPKPEPAVPVPAPPGRLPEPATD-----HAAGHPTPRPRPREPH-- 317
QY 375 EHDDPSPDDYYNMDPAVI-----PVEETTKSSNAVS---MPIFAFVACALVG 422
D 318 ---RPPAP-----PAVVPSSGMPQAPAPFPQPRTPAAGVSRHSVIVGTGTMGALLVG 367
QY 423 LLVW 426
D 368 VCVY 371

RESULT 13
Q91W00 PRELIMINARY; PRT; 516 AA.
AC Q91W00;
DT 01-OCT-2000 (TReMBLrel_15 Created)
DI 01-OCT-2000 (TReMBLrel_15, Last sequence update)
PT 01-JUN-2002 (TReMBLrel_21, Last annotation update)
DE Hybrid protein.
GN MUTANT GDIE.
OS Pseudorabies virus (strain Kaplan) (PRV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicelloviruses.
OX NCBI_TaxID=33703;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KAPLAN;
RX MEDLINE=20219392; PubMed=10756012;
RA Brack A.R., Klump B.G., Granzow H., Tirabassi R., Enquist L.W.,
RA Mettenleiter T.C.;
RT "Role of the cytoplasmic tail of pseudorabies virus glycoprotein e in
RT virus formation.";
RL J. Virol. 74:4004-4016(2000).
DR EMBL: AJ271967; CAB72452.1; -.
DR InterPro: IPR003404; Herpes_glycop.
DR InterPro: IPR002896; Herpes_glycop.
DR InterPro: IPR002965; P_rich_extensn.
DR Pfam: PF02480; Herpes_gE; 1.
DR Pfam: PF01537; Herpes_glycop_D; 1.
DR PRINTS: PR01217; PRICHEXTENSN.
SQ SEQUENCE 516 AA; 56874 MW; 87312C43E7E7FED CRC64;

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## OM protein - protein search, using sw model

Run on: February 19, 2003, 16:21:11 ; Search time 18 seconds

(without alignments)  
709,419 Million cell updates/sec

Title: US-09-994-064-11

Sequence: 1 MRRPHLRHRSRYAKGEVLN.....ACAVALVGLWSTVWCARS 434

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2311	100.0	434	2	US-08-484-575A-20 Sequence 20, Appl
2	2311	100.0	434	3	US-08-477-459-20 Sequence 20, Appl
3	2311	100.0	434	3	US-08-479-869-20 Sequence 20, Appl
4	2311	100.0	434	4	US-08-486-414-46 Sequence 46, Appl
5	2311	100.0	434	5	PCT-US94-01826A-20 Sequence 20, Appl
6	2311	100.0	434	5	PCT-US94-02252A-20 Sequence 20, Appl
7	2311	100.0	434	5	PCT-US96-03916-11 Sequence 11, Appl
8	2311	100.0	434	5	PCT-US96-03916-67 Sequence 67, Appl
9	772	33.4	144	4	US-08-486-414-20 Sequence 20, Appl
10	196	8.5	393	1	US-08-220-151-23 Sequence 23, Appl
11	196	8.5	393	1	US-08-413-118-23 Sequence 23, Appl
12	196	8.5	393	3	US-08-473-446-23 Sequence 23, Appl
13	190	8.2	369	2	US-08-139-609-1 Sequence 1, Appl
14	190	8.2	394	1	US-08-499-568-4 Sequence 4, Appl
15	190	8.2	394	2	US-08-793-958-4 Sequence 4, Appl
16	184.5	8.0	442	6	5470718-2 Patent No. 5470718
17	183.5	7.9	393	6	5162195-10 Patent No. 5162195
18	181.5	7.9	393	6	5470718-5 Patent No. 5470718
19	181	7.8	442	1	US-08-220-151-22 Sequence 22, Appl
20	181	7.8	442	1	US-08-413-118-22 Sequence 22, Appl
21	181	7.8	442	3	US-08-473-446-22 Sequence 22, Appl
22	181	7.8	442	6	5470718-3 Patent No. 5470718
23	179	7.7	388	1	US-08-499-568-11 Sequence 11, Appl
24	179	7.7	388	2	US-08-793-958-11 Sequence 11, Appl
25	165.5	7.2	308	2	US-08-499-568-2 Sequence 2, Appl
26	165.5	7.2	308	2	US-08-793-958-2 Sequence 2, Appl
27	165	7.1	402	6	5352575-5 Patent No. 5352575

## ALIGNMENTS

```
RESULT 1
US-08-484-575A-20
; Sequence 20, Application US/08484575A
; Patent No. 5925358
; GENERAL INFORMATION:
; APPLICANT: Mark D. Cochran and David E. Junker
; TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses Thereof
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,575A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)278-0450
; TELEFAX: (212)391-0525
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 434 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-484-575A-20

Query Match      100.0%; Score 2311; DB 2; Length 434;
Best Local Similarity 100.0%; Pred. No. 4e-233;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRPHLRHRSRYAKGEVLNKHNDGCGKRCGSAVFTLFWTCVRIMREHICVRNAMDR 60
Db 1 MRRPHLRHRSRYAKGEVLNKHNDGCGKRCGSAVFTLFWTCVRIMREHICVRNAMDR 60
QY 61 HLELRNFWITVLLSFAQSSTAATVYDITLGRALDALTIIPAVGPNRYLTRVSGCOV 120
Db 61 HLELRNFWITVLLSFAQSSTAATVYDITLGRALDALTIIPAVGPNRYLTRVSGCOV 120
QY 121 VELNPTISNVDDMTLSAKKREKGFPEASVYWFIVIGDGDGDKCYPIYRKREYRCDQVL 180
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Db 121 VELNPISNVDDMTSAAKEKEKGPFEASVYWFYVIKGDGEDKCPYRREKRECGDVOL 180
OY 181 LSCAQAOSAMWADVVPSTLVSRNAGLTIPTALSGOYLTLTKIGRPAOTALVTL 240
Db 181 LSCAQAOSAMWADVVPSTLVSRNAGLTIPTALSGOYLTLTKIGRPAOTALVTL 240
OY 241 VDRCLKIGSQLNLFPSKCMTEQYOTGFQGEHLPIADJNTRHADVDYRGYEDILQRMN 300
Db 241 VDRCLKIGSQLNLFPSKCMTEQYOTGFQGEHLPIADJNTRHADVDYRGYEDILQRMN 300
OY 301 NLIRKKNPSAPDRPDSVPOEIPAVTKKAGRTPPAESSEKKAPPEDESDMOAASGEN 360
Db 301 NLIRKKNPSAPDRPDSVPOEIPAVTKKAGRTPPAESSEKKAPPEDESDMOAASGEN 360
OY 361 PALPEDEVPEDTEHDDPNSDPDYNDMPAVIPVEETKSSNAVSMPIFAAFVACAVAL 420
Db 361 PALPEDEVPEDTEHDDPNSDPDYNDMPAVIPVEETKSSNAVSMPIFAAFVACAVAL 420
OY 421 VGLLWMSIVKARS 434
Db 421 VGLLWMSIVKARS 434

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## RESULT 2

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US-08-477-459-20
; Sequence 20, Application US/08477459
; Patent No. 6001369
; GENERAL INFORMATION:
; APPLICANT: Mark D. Cochran
; TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses
; TITLE OF INVENTION: Theoret
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,459
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 434 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-477-459-20

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Query Match 100.0%; Score 2311; DB 3; Length 434;
Best Local Similarity 100.0%; Pred. No. 4e-233;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MHRPLRHSRYAKGEVLNKHMDGGRCCGAAVFTLFWTCVIRREHICFVRNAMD 60
Db 1 MHRPLRHSRYAKGEVLNKHMDGGRCCGAAVFTLFWTCVIRREHICFVRNAMD 60
OY 61 HLFLRNATWITVLSSFSASQSTAAVTYDIILGRALDALTTIPAVGPYRYLTRSRGCV 120
Db 61 HLFLRNATWITVLSSFSASQSTAAVTYDIILGRALDALTTIPAVGPYRYLTRSRGCV 120

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OY 121 VELNPISNVDDMTSAAKEKEKGPFEASVYWFYVIKGDGEDKCPYRREKRECGDVOL 180
Db 121 VELNPISNVDDMTSAAKEKEKGPFEASVYWFYVIKGDGEDKCPYRREKRECGDVOL 180
OY 181 LSCAQAOSAMWADVVPSTLVSRNAGLTIPTALSGOYLTLTKIGRPAOTALVTL 240
Db 181 LSCAQAOSAMWADVVPSTLVSRNAGLTIPTALSGOYLTLTKIGRPAOTALVTL 240
OY 241 VDRCLKIGSQLNLFPSKCMTEQYOTGFQGEHLPIADJNTRHADVDYRGYEDILQRMN 300
Db 241 VDRCLKIGSQLNLFPSKCMTEQYOTGFQGEHLPIADJNTRHADVDYRGYEDILQRMN 300
OY 301 NLIRKKNPSAPDRPDSVPOEIPAVTKKAGRTPPAESSEKKAPPEDESDMOAASGEN 360
Db 301 NLIRKKNPSAPDRPDSVPOEIPAVTKKAGRTPPAESSEKKAPPEDESDMOAASGEN 360
OY 361 PALPEDEVPEDTEHDDPNSDPDYNDMPAVIPVEETKSSNAVSMPIFAAFVACAVAL 420
Db 361 PALPEDEVPEDTEHDDPNSDPDYNDMPAVIPVEETKSSNAVSMPIFAAFVACAVAL 420
OY 421 VGLLWMSIVKARS 434
Db 421 VGLLWMSIVKARS 434

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## RESULT 3

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US-08-479-869-20
; Sequence 20, Application US/08479869
; Patent No. 6123949
; GENERAL INFORMATION:
; APPLICANT: Cochran Ph.D, Mark D
; TITLE OF INVENTION: Recombinant Fowlpox Virus S-FPV-043 and
; TITLE OF INVENTION: Uses Thereof
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,869
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/024,156
; FILING DATE: 26-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)977-9550
; TELEFAX: (212)664-0525
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 434 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-479-869-20

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Query Match 100.0%; Score 2311; DB 3; Length 434;
Best Local Similarity 100.0%; Pred. No. 4e-233;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MHRPLRHSRYAKGEVLNKHMDGGRCCGAAVFTLFWTCVIRREHICFVRNAMD 60

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Db 1 MHRPLRRHSRYAKGEVLNKHMDCCGKRCSSGAAVFTLFWTCVIRREHICFVRNAMD 60
Qy 61 HLFIRNAFWTIVLLSSFASSOSTAAVTYDYLIGRRALDALTPAVGPNRYLTRVSRGCV 120
Db 61 HLFIRNAFWTIVLLSSFASSOSTAAVTYDYLIGRRALDALTPAVGPNRYLTRVSRGCV 120
Qy 121 VELNPISNVDMISAAREKEGKGFPEASVWFYIKGDGDEDKYCPYRREYREGCDVOL 180
Db 121 VELNPISNVDMISAAREKEGKGFPEASVWFYIKGDGDEDKYCPYRREYREGCDVOL 180
Qy 181 LSECAGSAGMMWADVSTVSRNGAGLTIFSPALSGOYLTLTKIGRFAQTALVTL 240
Db 181 LSECAGSAGMMWADVSTVSRNGAGLTIFSPALSGOYLTLTKIGRFAQTALVTL 240
Qy 241 VNRCLKIGSOLNLPSCKMTTEQYQTFQGEHLYPADNTNRHADVYRGYEDILGRMN 300
Db 241 VNRCLKIGSOLNLPSCKMTTEQYQTFQGEHLYPADNTNRHADVYRGYEDILGRMN 300
Qy 301 NLKRKNPSADPPRDSVPQEIIPAVTKKAEGRTPDAESSEKKAPPESEDDMOAEASGEN 360
Db 301 NLKRKNPSADPPRDSVPQEIIPAVTKKAEGRTPDAESSEKKAPPESEDDMOAEASGEN 360
Qy 361 PALPEDEVEDTEHDDPNSDPYNDMPAVIPVEETTKSSNAVSMPIFAFVACAVAL 420
Db 361 PALPEDEVEDTEHDDPNSDPYNDMPAVIPVEETTKSSNAVSMPIFAFVACAVAL 420
Qy 421 VGLLWSTIVKCARS 434
Db 421 VGLLWSTIVKCARS 434
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RESULT 4
US-08-486-414-46
: Sequence 46, Application US/08486414B
: Patent No. 6136318
: GENERAL INFORMATION:
: APPLICANT: Cochran, Mark D.
: APPLICANT: Junker, David E.
: TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUSES AND USES THEREOF
: FILE REFERENCE: 42771D
: CURRENT APPLICATION NUMBER: US/08/486,414B
: CURRENT FILING DATE: 1995-06-07
: NUMBER OF SEQ ID NOS: 46
: SOFTWARE: Patentin Ver. 2.1
: SEQ ID NO 46
: LENGTH: 434
: TYPE: PRT
: ORGANISM: Fowlpox virus
US-08-486-414-46
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Query Match 100.0%; Score 2311; DB 4; Length 434;  
Best Local Similarity 100.0%; Pred. No. 4e-233;  
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MHRPLRRHSRYAKGEVLNKHMDCCGKRCSSGAAVFTLFWTCVIRREHICFVRNAMD 60
Db 1 MHRPLRRHSRYAKGEVLNKHMDCCGKRCSSGAAVFTLFWTCVIRREHICFVRNAMD 60
Qy 61 HLFIRNAFWTIVLLSSFASSOSTAAVTYDYLIGRRALDALTPAVGPNRYLTRVSRGCV 120
Db 61 HLFIRNAFWTIVLLSSFASSOSTAAVTYDYLIGRRALDALTPAVGPNRYLTRVSRGCV 120
Qy 121 VELNPISNVDMISAAREKEGKGFPEASVWFYIKGDGDEDKYCPYRREYREGCDVOL 180
Db 121 VELNPISNVDMISAAREKEGKGFPEASVWFYIKGDGDEDKYCPYRREYREGCDVOL 180
Qy 181 LSECAGSAGMMWADVSTVSRNGAGLTIFSPALSGOYLTLTKIGRFAQTALVTL 240
Db 181 LSECAGSAGMMWADVSTVSRNGAGLTIFSPALSGOYLTLTKIGRFAQTALVTL 240
Qy 241 VNRCLKIGSOLNLPSCKMTTEQYQTFQGEHLYPADNTNRHADVYRGYEDILGRMN 300
Db 241 VNRCLKIGSOLNLPSCKMTTEQYQTFQGEHLYPADNTNRHADVYRGYEDILGRMN 300
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Db 241 VNRCLKIGSOLNLPSCKMTTEQYQTFQGEHLYPADNTNRHADVYRGYEDILGRMN 300
Qy 301 NLKRKNPSADPPRDSVPQEIIPAVTKKAEGRTPDAESSEKKAPPESEDDMOAEASGEN 360
Db 301 NLKRKNPSADPPRDSVPQEIIPAVTKKAEGRTPDAESSEKKAPPESEDDMOAEASGEN 360
Qy 361 PALPEDEVEDTEHDDPNSDPYNDMPAVIPVEETTKSSNAVSMPIFAFVACAVAL 420
Db 361 PALPEDEVEDTEHDDPNSDPYNDMPAVIPVEETTKSSNAVSMPIFAFVACAVAL 420
Qy 421 VGLLWSTIVKCARS 434
Db 421 VGLLWSTIVKCARS 434
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RESULT 5
PCT-US94-01826A-20
: Sequence 20, Application PC/TUS9401826A
: GENERAL INFORMATION:
: APPLICANT: Syntro Corporation, et al.
: TITLE OF INVENTION: Recombinant Fowlpox Virus S-FPV-043 and Uses Thereof
: NUMBER OF SEQUENCES: 20
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: John P. White
: STREET: 30 Rockefeller Plaza
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10112
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/01826A
: FILING DATE: 28-FEB-1994
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: White Esq, John P
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212)977-9950
: TELEFAX: (212)664-0525
: TELEX: 422323
: INFORMATION FOR SEQ ID NO: 20:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 434 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
PCT-US94-01826A-20
```

Query Match 100.0%; Score 2311; DB 5; Length 434;  
Best Local Similarity 100.0%; Pred. No. 4e-233;  
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 1 MHRPLRRHSRYAKGEVLNKHMDCCGKRCSSGAAVFTLFWTCVIRREHICFVRNAMD 60
Db 1 MHRPLRRHSRYAKGEVLNKHMDCCGKRCSSGAAVFTLFWTCVIRREHICFVRNAMD 60
Qy 61 HLFIRNAFWTIVLLSSFASSOSTAAVTYDYLIGRRALDALTPAVGPNRYLTRVSRGCV 120
Db 61 HLFIRNAFWTIVLLSSFASSOSTAAVTYDYLIGRRALDALTPAVGPNRYLTRVSRGCV 120
Qy 121 VELNPISNVDMISAAREKEGKGFPEASVWFYIKGDGDEDKYCPYRREYREGCDVOL 180
Db 121 VELNPISNVDMISAAREKEGKGFPEASVWFYIKGDGDEDKYCPYRREYREGCDVOL 180
Qy 181 LSECAGSAGMMWADVSTVSRNGAGLTIFSPALSGOYLTLTKIGRFAQTALVTL 240
Db 181 LSECAGSAGMMWADVSTVSRNGAGLTIFSPALSGOYLTLTKIGRFAQTALVTL 240
Qy 241 VNRCLKIGSOLNLPSCKMTTEQYQTFQGEHLYPADNTNRHADVYRGYEDILGRMN 300
Db 241 VNRCLKIGSOLNLPSCKMTTEQYQTFQGEHLYPADNTNRHADVYRGYEDILGRMN 300
```

Db 241 VNRCLKIGSOLNLPSCWTEYOYOTGFOGHEHLYPIADINTRHADVYRGEDILQRMN 300  
QY 301 NLRRKNPSADPPRDSVPOEIPAVTKKAGRTPDASESSKKAPPESEDDMOAASGEN 360  
Db 301 NLRRKNPSADPPRDSVPOEIPAVTKKAGRTPDASESSKKAPPESEDDMOAASGEN 360  
QY 361 PALPEDEVEPEDEHDDPNSDPDYNDMPAVIPEETTKSSNAVSMPIFAAFVACAVALL 420  
Db 361 PALPEDEVEPEDEHDDPNSDPDYNDMPAVIPEETTKSSNAVSMPIFAAFVACAVALL 420  
QY 421 VGLLWSTIVKCAR 434  
Db 421 VGLLWSTIVKCAR 434

RESULT 6  
PCT-US94-02252A-20

Sequence 20, Application PC/TUS9402252A  
GENERAL INFORMATION:  
APPLICANT: Syntro Corporation, et al.  
TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses Thereof  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/02252A  
FILING DATE: 28-FEB-1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: White Esq. John P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)977-9550  
TELEFAX: (212)664-0525  
TELEX: 422523  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 434 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US94-02252A-20

Query Match 100.0%; Score 2311; DB 5; Length 434;  
Best Local Similarity 100.0%; Pred. No. 4e-233;  
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRPHLRHSRYAKGEVLNKHMDGCGKRCGSAAVFTLFWTCVRLMREHICFVRNADR 60  
Db 1 MHRPHLRHSRYAKGEVLNKHMDGCGKRCGSAAVFTLFWTCVRLMREHICFVRNADR 60  
QY 61 HFLRNAFTIYLLSSFASSOSTAAVTYDYLGRALDALITPAVGPNRYLFRVSGCDV 120  
Db 61 HFLRNAFTIYLLSSFASSOSTAAVTYDYLGRALDALITPAVGPNRYLFRVSGCDV 120  
QY 121 VELNPISNVDDMISAKEKEKGPEASVWVFYIKGDDGEGKCYCPYRKREYREGCDV 180  
Db 121 VELNPISNVDDMISAKEKEKGPEASVWVFYIKGDDGEGKCYCPYRKREYREGCDV 180  
QY 181 LSECAVQASQAMNAVDPVSTLVSRRNGAGLITSPALSGOYLTLTKIRPOTALTVE 240  
Db 181 LSECAVQASQAMNAVDPVSTLVSRRNGAGLITSPALSGOYLTLTKIRPOTALTVE 240

QY 241 VNRCLKIGSOLNLPSCWTEYOYOTGFOGHEHLYPIADINTRHADVYRGEDILQRMN 300  
Db 241 VNRCLKIGSOLNLPSCWTEYOYOTGFOGHEHLYPIADINTRHADVYRGEDILQRMN 300  
QY 301 NLRRKNPSADPPRDSVPOEIPAVTKKAGRTPDASESSKKAPPESEDDMOAASGEN 360  
Db 301 NLRRKNPSADPPRDSVPOEIPAVTKKAGRTPDASESSKKAPPESEDDMOAASGEN 360  
QY 361 PALPEDEVEPEDEHDDPNSDPDYNDMPAVIPEETTKSSNAVSMPIFAAFVACAVALL 420  
Db 361 PALPEDEVEPEDEHDDPNSDPDYNDMPAVIPEETTKSSNAVSMPIFAAFVACAVALL 420  
QY 421 VGLLWSTIVKCAR 434  
Db 421 VGLLWSTIVKCAR 434

RESULT 7  
PCT-US96-03916-11

Sequence 11, Application PC/TUS9603916  
GENERAL INFORMATION:  
APPLICANT: Wild, Martha A.  
TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/03916  
FILING DATE: 23-MAR-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/126,597  
FILING DATE: 24-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 39116-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 434 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US96-03916-11

Query Match 100.0%; Score 2311; DB 5; Length 434;  
Best Local Similarity 100.0%; Pred. No. 4e-233;  
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRPHLRHSRYAKGEVLNKHMDGCGKRCGSAAVFTLFWTCVRLMREHICFVRNADR 60  
Db 1 MHRPHLRHSRYAKGEVLNKHMDGCGKRCGSAAVFTLFWTCVRLMREHICFVRNADR 60  
QY 61 HFLRNAFTIYLLSSFASSOSTAAVTYDYLGRALDALITPAVGPNRYLFRVSGCDV 120  
Db 61 HFLRNAFTIYLLSSFASSOSTAAVTYDYLGRALDALITPAVGPNRYLFRVSGCDV 120  
QY 121 VELNPISNVDDMISAKEKEKGPEASVWVFYIKGDDGEGKCYCPYRKREYREGCDV 180

Db 121 VELNPISVNDMISAKEKEGPFESVWFYIKGDDGDKCPIYRKREYRCGCVOL 180  
QY 181 LSECAVSAOMWADVPSYVSTLVSRNAGLTFISPTALSGOYLTLTKIGRPAQTALVLE 240  
Db 181 LSECAVSAOMWADVPSYVSTLVSRNAGLTFISPTALSGOYLTLTKIGRPAQTALVLE 240  
QY 241 VNDCLKIGSQLNLPKSCWTEQYOTGFOGHEHLYPIADNTRHADVYRGYEDIIQRMN 300  
Db 241 VNDCLKIGSQLNLPKSCWTEQYOTGFOGHEHLYPIADNTRHADVYRGYEDIIQRMN 300  
QY 301 NLKRNKPSAPDPRDSVPQEIPIAVYTKKAGRTPDASSEKKAPPEDEDDMOAASGEN 360  
Db 301 NLKRNKPSAPDPRDSVPQEIPIAVYTKKAGRTPDASSEKKAPPEDEDDMOAASGEN 360  
QY 361 PALPEDEVEPDETHDHPNSDPDYNDMPAVIPEETTKSSNAVSMPIFAFVACAVAL 420  
Db 361 PALPEDEVEPDETHDHPNSDPDYNDMPAVIPEETTKSSNAVSMPIFAFVACAVAL 420  
QY 421 VGLLWMSIVKARS 434  
Db 421 VGLLWMSIVKARS 434

RESULT 8  
PCT-US96-03916-67

; Sequence 67, Application PC/TUS9603916  
; GENERAL INFORMATION:  
; APPLICANT: Wild, Martha A.  
; APPLICANT: Cochran, Mark D.  
; TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS  
; TITLE OF INVENTION: AND USES THEREOF  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/03916  
; FILING DATE: 23-MAR-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/126,597  
; FILING DATE: 24-SEP-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 39116-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; INFORMATION FOR SEQ ID NO: 67:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 434 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; PCT-US96-03916-67

Query Match 100.0%; Score 2311; DB 5; Length 434;  
Best Local Similarity 100.0%; Pred. No. 4e-233;  
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MHRPHLRHRSRYAKGEVLNKHMDGGRCCSGAAVFTLFWTCVRIMREHICFVRNAMD 60  
|||||

Db 1 MHRPHLRHRSRYAKGEVLNKHMDGGRCCSGAAVFTLFWTCVRIMREHICFVRNAMD 60  
QY 61 HLFRLNMFMTIVLLSFASTASTAAYTYDYLIGRRALDALTPAVGPNRYLTRVSRGCV 120  
Db 61 HLFRLNMFMTIVLLSFASTASTAAYTYDYLIGRRALDALTPAVGPNRYLTRVSRGCV 120  
QY 121 VELNPISVNDMISAKEKEGPFESVWFYIKDDGDKCPIYRKREYRCGCVOL 180  
Db 121 VELNPISVNDMISAKEKEGPFESVWFYIKDDGDKCPIYRKREYRCGCVOL 180  
QY 181 LSECAVSAOMWADVPSYVSTLVSRNAGLTFISPTALSGOYLTLTKIGRPAQTALVLE 240  
Db 181 LSECAVSAOMWADVPSYVSTLVSRNAGLTFISPTALSGOYLTLTKIGRPAQTALVLE 240  
QY 241 VNDCLKIGSQLNLPKSCWTEQYOTGFOGHEHLYPIADNTRHADVYRGYEDIIQRMN 300  
Db 241 VNDCLKIGSQLNLPKSCWTEQYOTGFOGHEHLYPIADNTRHADVYRGYEDIIQRMN 300  
QY 301 NLKRNKPSAPDPRDSVPQEIPIAVYTKKAGRTPDASSEKKAPPEDEDDMOAASGEN 360  
Db 301 NLKRNKPSAPDPRDSVPQEIPIAVYTKKAGRTPDASSEKKAPPEDEDDMOAASGEN 360  
QY 361 PALPEDEVEPDETHDHPNSDPDYNDMPAVIPEETTKSSNAVSMPIFAFVACAVAL 420  
Db 361 PALPEDEVEPDETHDHPNSDPDYNDMPAVIPEETTKSSNAVSMPIFAFVACAVAL 420  
QY 421 VGLLWMSIVKARS 434  
Db 421 VGLLWMSIVKARS 434

RESULT 9  
US-08-486-414-20

; Sequence 20, Application US/08486414B  
; Patent No. 6136318  
; GENERAL INFORMATION:  
; APPLICANT: Cochran, Mark D.  
; APPLICANT: Junker, David E.  
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUSES AND USES THEREOF  
; FILE REFERENCE: 42771D  
; CURRENT APPLICATION NUMBER: US/08/486,414B  
; CURRENT FILING DATE: 1995-06-07  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 144  
; TYPE: PR1  
; ORGANISM: Fowlpox virus  
; US-08-486-414-20

Query Match 33.4%; Score 772; DB 4; Length 144;  
Best Local Similarity 100.0%; Pred. No. 6.9e-73;  
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRPHLRHRSRYAKGEVLNKHMDGGRCCSGAAVFTLFWTCVRIMREHICFVRNAMD 60  
Db 1 MHRPHLRHRSRYAKGEVLNKHMDGGRCCSGAAVFTLFWTCVRIMREHICFVRNAMD 60  
QY 61 HLFRLNMFMTIVLLSFASTASTAAYTYDYLIGRRALDALTPAVGPNRYLTRVSRGCV 120  
Db 61 HLFRLNMFMTIVLLSFASTASTAAYTYDYLIGRRALDALTPAVGPNRYLTRVSRGCV 120  
QY 121 VELNPISVNDMISAKEKEGPFESVWFYIKDDGDKCPIYRKREYRCGCVOL 180  
Db 121 VELNPISVNDMISAKEKEGPFESVWFYIKDDGDKCPIYRKREYRCGCVOL 180  
QY 144 VELNPISVNDMISAKEKEGPFESVWFYIKDDGDKCPIYRKREYRCGCVOL 144  
Db 144 VELNPISVNDMISAKEKEGPFESVWFYIKDDGDKCPIYRKREYRCGCVOL 144

RESULT 10  
US-08-220-151-23  
; Sequence 23, Application US/08220151  
; Patent No. 5529780  
; GENERAL INFORMATION:  
; APPLICANT: Paoletti, Enzo

```

? APPLICANT: LIMBACH, KEITH J.
? TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES OF
? TITLE OF INVENTION: CANINE HERPESVIRUS gB, gC, AND gD AND USES THEREFOR
? NUMBER OF SEQUENCES: 128
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.
? STREET: 530 FIFTH AVENUE, 25TH FLOOR
? CITY: NEW YORK
? STATE: NEW YORK
? COUNTRY: UNITED STATES OF AMERICA
? ZIP: 10036
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/413,118
? FILING DATE: 29-MAR-1995
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/220,151
? FILING DATE: 30-MAR-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: FROMMER, WILLIAM S.
? REGISTRATION NUMBER: 25,506
? REFERENCE/DOCKET NUMBER: 454310-2670
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (212) 840-3333
? TELEFAX: (212) 840-0712
? INFORMATION FOR SEQ ID NO: 23:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 393 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? FRAGMENT TYPE: N-terminal
?
US-08-413-118-23

Query Match      8.5%; Score 196; DB 1; Length 393;
Best Local Similarity 24.0%; Pred. No. 6.7e-12;
Matches 79; Conservative 46; Mismatches 138; Indels 66; Gaps 14;

OY 113 RVSRCDDVVELMPISNVDMISAAREKEKGGFEASVWFYIKGDGDXCKPTRYREX 172
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 85 RVERNCRSVLNAPSEAPQIVGASDVAKOPYNTLIANFRM-----GCNCALPIVMXY 139
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 173 RECGVDYLISECAVOAQMMAVDVPS-FLVSRNGAGLTIFSPTALSGQYLLTIKTGRF 231
    :||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 140 TECSYNKSIGACPIRTOPRW--NYDSFSVASSEDNLGFIMHAPAFETACTYLRVKINDW 197
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 232 AQTALVTLE--VNDRCLIKGSOLNFLPSKCMTTEQYONG-----FGGHLYPLA 278
    :||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 198 TETITFILEHRKKSGC-KYTLEPLRPSSACLSPQAIQQGVYVDSIGMLPRFIENQRTVA 256
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 279 DITNRHADVVYRGYEDIIQRNMNNLRRKNPSAPDRPRSVPQEIPAVTAKKAAGRTPDAES 338
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 257 VYSLKTAG-----WH-----GPRAP-YTSTLLPELP-----ETPNM-- 287
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 339 SEKKARPDESDSD-WQAASAENGPAALBEDDEVEDTETHDPNSPPDYIYNDKPAVIYPVEE 397
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 288 TOPELAPADPDPESSALLEPDVGTVAPQIPPMNHIPSIODAAATPYHPBPATPINMGILI----- 342
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 398 TTSSNAVSMPIFAFVACAVALLGW 426
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 343 ----AGAVGGSLMALVIC-----GIYYM 362
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 12
US-08-473-446-23
Sequence 23, Application US/08473446
Patent No. 6017542
```

GENERAL INFORMATION:  
APPLICANT: PAOLETTI, ENZO  
TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES OF  
TITLE OF INVENTION: CANINE HERPESVIRUS gB, gC, AND gD AND USES THEREFOR  
NUMBER OF SEQUENCES: 128  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.  
STREET: 530 FIFTH AVENUE, 25TH FLOOR  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/473,446  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/413,118  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: FROMMER, WILLIAM S.  
REGISTRATION NUMBER: 25,506  
REFERENCE/DOCKET NUMBER: 454310-2670  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 393 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: N-terminal  
US-08-473-446-23

Query Match 8.5%; Score 196; DB 3; Length 393;  
Best Local Similarity 24.0%; Pred. No. 6.7e-12;  
Matches 79; Conservative 46; Mismatches 138; Indels 66; Gaps 14;

113 RVRGCDVVELNPNISVNDMISAKEKEKGPEASVWVFYIKGDGEDKCYPIYKEY 172  
113 RVRGCDVVELNPNISVNDMISAKEKEKGPEASVWVFYIKGDGEDKCYPIYKEY 172  
85 RVRGCDVVELNPNISVNDMISAKEKEKGPEASVWVFYIKGDGEDKCYPIYKEY 139  
173 REGCDVQLSECAVQSAQMAVAVDVPVPS-TLVSRNGAGLTFFSPTAALSGOYLTLKIGRF 231  
140 TEGSYNKSGLACPIRQPRM--NYVDSFSAVSEDNLGLHMAFAFETAGTYLRLKINDW 197  
232 AQAALVLE--VNDRLKIGSOLNPLPSKWTTEOYQTG-----FQGBHLPIA 278  
198 TETTOFLERAKGSC-KYTLPLRIPPSACLSQAAYOQGVTVDSIGMLPRFIFENQRTVA 256  
279 DVTMTRHADVDYRGVEDILQRMNMLLRKKNPSPADPRDVSPOEIPAVTKKAEGSTPAES 338  
257 VYSLKLAG-----WH-----GPRAP-YSTILLPELP-----ETPNA-- 287  
339 SEKKAPPESEDD--MQAASGENPALPEDEVEPDETHDDPNSDDPYNDMPAVIPEVE 397  
288 TOELAPPEDEDSALLEDPVGAQIPRMWHPISIODATPYHPRATPNNMGLI----- 342  
398 TTKSSNAVMPITAFYACAVALVGLLW 426  
343 ---AGAVGSLAALVLC-----GIYVW 362

RESULT 13  
US-08-139-609-1

Sequence 1, Application US/08139609  
Patent No. 5837249  
GENERAL INFORMATION:  
APPLICANT: Heber-Katz, Ellen  
TITLE OF INVENTION: Dietzschold, Bernhard  
TITLE OF INVENTION: Method for Generating an Immunogenic T  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howson and Howson  
STREET: Spring House Corporate Cntr., P.O. Box 457  
CITY: Spring House  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19477  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/139,609  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/868,946  
FILING DATE: 15-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/685,459  
FILING DATE: 12-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/047,443  
FILING DATE: 08-MAY-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 06/725,087  
FILING DATE: 19-APR-1985  
ATTORNEY/AGENT INFORMATION:  
NAME: Bak, Mary E.  
REGISTRATION NUMBER: 31,215  
REFERENCE/DOCKET NUMBER: WSTIDUSA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-540-9200  
TELEFAX: 215-540-5818  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 369 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-139-609-1

Query Match 8.2%; Score 190; DB 2; Length 369;  
Best Local Similarity 23.2%; Pred. No. 2.6e-11;  
Matches 78; Conservative 47; Mismatches 145; Indels 66; Gaps 14;

106 PYRKYLRVSGCDVVELNPNISVNDMISAKEKEKGPEASVWVFYIKGDGEDKCY 165  
54 PITVYVAVLERACRSVYLLNAPSEAPQIVRGASEDVKQPYNTLIAMFRM-----GGNCAL 108  
166 PIYRKEYREGCDVQLSECAVQSAQMAVAVDVPVPS-TLVSRNGAGLTFFSPTAALSGOYL 224  
109 PITVYETECYSKSLGACPIRQPRM--NYVDSFSAVSEDNLGLHMAFAFETAGTYLRL 166  
225 TLKIGRAQALVLE--VNDRLKIGSOLNPLPSKWTTEOYQTG-----FQGBHLPIA 271  
167 LVKINDWTELTQFLERAKGSC-KYALPLRIPPSACLSQAAYOQGVTVDSIGMLRFRIF 225  
272 EHLYPADNTMTRHADVDYRGVEDILQRMNMLLRKKNPSPADPRDVSPOEIPAVTKKAEG 331  
226 ENQRTVAVYSLKLAG-----WH-----GPRAP-YSTILLPELP-----S 258  
332 RTPDASESEKKAPPESEDD--MQAASGENPALPEDEVEPDETHDDPNSDDPYNDMP 390

Db 259 ETNNA--TOPELAPEDPEDSALLEDPYGTVAPOIPPMWHIPSIQDAPYHPHPATPNNMG 316  
QY 391 AVIPVEETKSSNAVSMPIFAFAVACALVGLLW 426  
Db 317 LI-----AGAVGSLIALALVIC-----GIVYW 338

## RESULT 14

US-08-499-568-4  
Sequence 4, Application US/08499568  
Patent No. 5654174  
GENERAL INFORMATION:  
APPLICANT: Cohen, Gary H.  
APPLICANT: Eisenberg, Roselyn J.  
APPLICANT: Nicola, Anthony  
TITLE OF INVENTION: Herpes Simplex Virus Glycoprotein D  
TITLE OF INVENTION: Variants  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 S. Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/499,568  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5654174and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 32813  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 394 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-499-568-4

Query Match 8.2%; Score 190; DB 1; Length 394;  
Best Local Similarity 23.2%; Pred. No. 2.9e-11;  
Matches 78; Conservative 47; Mismatches 145; Indels 66; Gaps 14;

QY 106 PYNRILTRSRRCGDVLEINPISNVDMISAKEKEKGFPEASVYVFYIKDDGDEKTC 165  
Db 79 PITYVAVYALERCRSVLLNAPSEAPQIVRGASEDVAKOPYNLTIMFRM-----GNCAL 133  
QY 166 PIYREYRECGDVOLLSECAVQSAQMMAVDVYPS--TIVSRNGAGITIPPTAALSGOYL 224  
Db 134 PITVMEYTEGCSYKSLGACPIRTQPRW--NYVDSFSAVSEDNIGLMAAPAFETAGTYLR 191  
QY 225 TLKIGRFQOTALVLE--VNDRCILIGSOLNPLPSKCTTQYOTG-----FOG 271  
Db 192 LVKINDWTEITQFILEHRAKQSC--KYALPLRIPPSACLSPOAYOGGVVDSIGMLPRFIP 250  
QY 272 EHLVPIATNTRHADVDYRGVEDILQKRNNLIRKKNPSAPDRPDSVPOELPATYKKAEG 331  
Db 251 ENQRTVAAYSLKIA-----WH-----GPKAP--YTSTLLPEL-----S 283  
QY 332 RTPDAESSEKRAPDESD--MQAEASGENPALPEDEVEPEDTEHDDPNSDPYNDMP 390  
Db 284 ETNNA--TOPELAPEDPEDSALLEDPYGTVAPOIPPMWHIPSIQDAPYHPHPATPNNMG 341

QY 391 AVIPVEETKSSNAVSMPIFAFAVACALVGLLW 426  
Db 342 LI-----AGAVGSLIALALVIC-----GIVYW 363

## RESULT 15

US-08-793-958-4  
Sequence 4, Application US/08793958  
Patent No. 5814486  
GENERAL INFORMATION:  
APPLICANT: Cohen, Gary H.  
APPLICANT: Eisenberg, Roselyn J.  
APPLICANT: Nicola, Anthony  
TITLE OF INVENTION: Herpes Simplex Virus Glycoprotein D  
TITLE OF INVENTION: Variants  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 S. Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/793,958  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/499,568  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5814486and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 32813  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 394 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-793-958-4

Query Match 8.2%; Score 190; DB 2; Length 394;  
Best Local Similarity 23.2%; Pred. No. 2.9e-11;  
Matches 78; Conservative 47; Mismatches 145; Indels 66; Gaps 14;

QY 106 PYNRILTRSRRCGDVLEINPISNVDMISAKEKEKGFPEASVYVFYIKDDGDEKTC 165  
Db 79 PITYVAVYALERCRSVLLNAPSEAPQIVRGASEDVAKOPYNLTIMFRM-----GNCAL 133  
QY 166 PIYREYRECGDVOLLSECAVQSAQMMAVDVYPS--TIVSRNGAGITIPPTAALSGOYL 224  
Db 134 PITVMEYTEGCSYKSLGACPIRTQPRW--NYVDSFSAVSEDNIGLMAAPAFETAGTYLR 191  
QY 225 TLKIGRFQOTALVLE--VNDRCILIGSOLNPLPSKCTTQYOTG-----FOG 271  
Db 192 LVKINDWTEITQFILEHRAKQSC--KYALPLRIPPSACLSPOAYOGGVVDSIGMLPRFIP 250  
QY 272 EHLVPIATNTRHADVDYRGVEDILQKRNNLIRKKNPSAPDRPDSVPOELPATYKKAEG 331  
Db 251 ENQRTVAAYSLKIA-----WH-----GPKAP--YTSTLLPEL-----S 283  
QY 332 RTPDAESSEKRAPDESD--MQAEASGENPALPEDEVEPEDTEHDDPNSDPYNDMP 390



Db 284 ETPNA--TOPELAPEDPEDSALLEDVGTVAPOIPPNWHIPSIQDATPYHPATPNMG 341  
QY 391 AVIPVEETKSSNAVSMPIFAFVACAVALVGLIW 426  
Db 342 LI-----AGAVGGSLALALVIC-----GIYYW 363

Search completed: February 19, 2003, 16:23:55  
Job time : 20 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 19, 2003, 16:23:39 ; Search time 13 Seconds

(without alignments)  
852.939 Million cell updates/sec

Title: US-09-994-064-11  
Perfect score: 2311  
Sequence: 1 MHRPHLRHSHRYAKGEVLN.....ACAAVGLVMSIVKCAR 434

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 25548876 residues  
Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubppaa/US08\_NEW\_PUB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubppaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubppaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubppaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubppaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/2/pubppaa/US07\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/2/pubppaa/PCTUS\_PUBCOMB.pep:\*
- 8: /cgn2\_6/ptodata/2/pubppaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/2/pubppaa/US09\_NEW\_PUB.pep:\*
- 10: /cgn2\_6/ptodata/2/pubppaa/US09\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/2/pubppaa/US10\_NEW\_PUB.pep:\*
- 12: /cgn2\_6/ptodata/2/pubppaa/US10\_PUBCOMB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubppaa/US60\_NEW\_PUB.pep:\*
- 14: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2311	100.0	434	10	US-09-881-457A-4
2	117	5.1	311	10	US-09-883-720-16
3	115	5.0	1648	10	US-09-515-806-4
4	112.5	4.9	305	10	US-09-883-720-12
5	110.5	4.8	302	10	US-09-883-720-14
6	110.5	4.8	1643	10	US-09-515-806-2
7	103.5	4.5	764	9	US-09-854-133-67
8	103.5	4.5	258	10	US-09-738-973-67
9	103	4.5	258	10	US-09-765-272-90
10	103	4.5	565	10	US-09-765-272-218
11	103	4.5	26926	9	US-09-759-5088-2
12	101	4.4	285	10	US-09-883-720-18
13	97.5	4.2	300	10	US-09-919-770-2
14	97	4.2	428	9	US-09-906-514-4
15	95.5	4.1	2462	9	US-09-819-104A-5
16	95	4.1	897	10	US-09-815-242-12769
17	95	4.1	1113	10	US-09-815-242-5836
18	94.5	4.1	314	10	US-09-206-576-2
19	94.5	4.1	356	10	US-09-791-961-3

20	94.5	4.1	2507	9	US-09-819-104A-2	Sequence 2, Appl1
21	94	4.1	508	10	US-09-016-159-5	Sequence 5, Appl1
22	94	4.1	1162	9	US-10-079-625-43	Sequence 43, Appl1
23	94	4.1	1198	10	US-09-866-582-36	Sequence 36, Appl1
24	94	4.1	1241	12	US-10-001-215-5	Sequence 5, Appl1
25	94	4.1	2485	10	US-09-802-669-46	Sequence 46, Appl1
26	93	4.0	254	10	US-09-126-193-126	Sequence 126, App
27	92.5	4.0	472	9	US-09-738-626-6752	Sequence 6752, App
28	91.5	4.0	423	9	US-09-738-626-5778	Sequence 3778, App
29	91.5	4.0	603	9	US-09-764-868-705	Sequence 705, App
30	91.5	4.0	763	10	US-09-765-272-66	Sequence 66, Appl1
31	91	3.9	545	10	US-09-967-624-5	Sequence 5, Appl1
32	90.5	3.9	488	10	US-09-925-300-1563	Sequence 1563, App
33	90	3.9	489	10	US-09-817-913-3	Sequence 3, Appl1
34	90	3.9	489	10	US-09-817-938-3	Sequence 3, Appl1
35	90	3.9	576	10	US-09-347-931-11	Sequence 11, Appl1
36	90	3.9	590	10	US-09-925-300-1219	Sequence 1219, App
37	89	3.9	265	12	US-10-073-256-78	Sequence 78, Appl1
38	89	3.9	863	9	US-10-016-634A-141	Sequence 141, App
39	88.5	3.8	577	9	US-10-029-180-48	Sequence 48, Appl1
40	88.5	3.8	693	10	US-09-752-639-154	Sequence 154, App
41	88.5	3.8	693	10	US-09-984-198-154	Sequence 154, App
42	88	3.8	214	10	US-09-214-881A-1	Sequence 1, Appl1
43	88	3.8	481	10	US-09-817-913-1	Sequence 1, Appl1
44	88	3.8	481	10	US-09-817-938-1	Sequence 1, Appl1
45	87.5	3.8	236	9	US-10-174-590-544	Sequence 544, App

## ALIGNMENTS

RESULT 1  
US-09-881-457A-4  
Sequence 4, Application US/09881457A  
Patent No. US20020081316A1  
GENERAL INFORMATION:  
APPLICANT: Cochran, Mark D  
APPLICANT: Cook, Stephanie M  
TITLE OF INVENTION: No. US20020081316A1el Avian Herpes Virus and Uses Thereof  
FILE REFERENCE: SY01105K10KOR  
CURRENT APPLICATION NUMBER: US/09/881,457A  
CURRENT FILING DATE: 2001-06-14  
PRIOR APPLICATION NUMBER: 09/426,352  
PRIOR FILING DATE: 1999-10-25  
PRIOR APPLICATION NUMBER: 08/804,372  
PRIOR FILING DATE: 1997-02-21  
PRIOR APPLICATION NUMBER: PCT/US95/10245  
PRIOR FILING DATE: 1995-08-09  
PRIOR APPLICATION NUMBER: 08/663,566  
PRIOR FILING DATE: 1996-06-13  
PRIOR APPLICATION NUMBER: 08/288,065  
PRIOR FILING DATE: 1994-08-09  
PRIOR APPLICATION NUMBER: PCT/US93/05681  
PRIOR FILING DATE: 1993-06-14  
PRIOR APPLICATION NUMBER: 08/023,610  
PRIOR FILING DATE: 1993-02-26  
PRIOR APPLICATION NUMBER: 07/898,087  
PRIOR FILING DATE: 1992-06-12  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 434  
TYPE: PRT  
ORGANISM: Infectious Laryngotracheitis Virus  
US-09-881-457A-4

Query Match 100.0%; Score 2311; DB 10; Length 434;  
Best Local Similarity 100.0%; Pred. No. 2.5e-191;  
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRPHLRHSHRYAKGEVLNKMDCGRCGCAAVFLFWCVIRMEHICFVRNMDR 60  
|||||

```

Db      1 MHRPIHRRSRYYANGVELINKHMDGCKRCSGAATLFWTCVHIMREHICFVHNAADR 60
QY      61 HLELRNAFWTIVLLSSFASTAAVTYDITLGRALDALTIPAVGPYNNYLRVSRGDY 120
Db      61 HLELRNAFWTIVLLSSFASTAAVTYDITLGRALDALTIPAVGPYNNYLRVSRGDY 120
QY      121 VELNPISNVDMISAKEKEKGPPEASVWVEYVIKGDGEDKCYPIYKREKRECGDYL 180
Db      121 VELNPISNVDMISAKEKEKGPPEASVWVEYVIKGDGEDKCYPIYKREKRECGDYL 180
QY      181 LSECAVOSQOMAVDYVSTIVSRNGAGITFSPALASGOYLITLKIGRAQALVLE 240
Db      181 LSECAVOSQOMAVDYVSTIVSRNGAGITFSPALASGOYLITLKIGRAQALVLE 240
QY      241 VNDRLCKIGSQLNPLPSKCMTEYOQOTGFOGHELYPIADTNTRHADVDYRGYEDILQWNN 300
Db      241 VNDRLCKIGSQLNPLPSKCMTEYOQOTGFOGHELYPIADTNTRHADVDYRGYEDILQWNN 300
QY      301 NLRRKNSAPDRPDSVPOEIPAVTKKAEGRTPDASESEKKAPPEDEDDMOAASGEN 360
Db      301 NLRRKNSAPDRPDSVPOEIPAVTKKAEGRTPDASESEKKAPPEDEDDMOAASGEN 360
QY      361 PALPEDEVEDPETHDDPNSDPDYNMPAVIPEEETKSSNAVSMPIFAAFVACAVAL 420
Db      361 PALPEDEVEDPETHDDPNSDPDYNMPAVIPEEETKSSNAVSMPIFAAFVACAVAL 420
QY      421 VGLLWSTIVKCAR 434
Db      421 VGLLWSTIVKCAR 434

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## RESULT 2

```

US-09-883-720-16
; Sequence 16, Application US/09883720
; Patent No. US20020022256A1
; GENERAL INFORMATION:
; APPLICANT: Baldwin, Donald A.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Crane, Virginia C.
; TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses
; FILE REFERENCE: 5718-44,
; CURRENT APPLICATION NUMBER: US/09/883,720
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/282,305
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Zea mays
; US-09-883-720-16

```

## Query Match

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Best Local Similarity 22.8%; Score 117; DB 10; Length 311;
Matches 56; Conservative 39; Mismatches 103; Indels 48; Gaps 10;

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QY      190 QMAVAVYVP-STIVSRNGAGITFSPALASGOYLITLKIGRAQALVLEVNDRLCKI 248
Db      2 EFWGLVKKGISTVCKCPHGFIHVSQAL-GE-----SKKSDALMYKVVDDKRLAI 53
QY      249 GS-----QLNF-----LPSKCMTEYOQOTGFOGHELYPIADTNTRHADVDYRGY 292
Db      54 GTLSIDKYQIQIDLVFNKEFELSHSKTTSVFSGYVEQ--PI-----EGDMDLDS 105
QY      293 EDILQWNNLNRKNSAPDRPDSVPOEIPAVTKKAEGRTPDASESEKKA 343
Db      106 EDEEBELNIPYIKENKAGKEKQKQKQKAVATAFKSKSLGEEKSKSDSDSDSDSD 165
QY      344 PEDSDDMQAVASGENPALPEDEVEDPETHDDPNSDPDYNMPAVIPEEETKSSN 403
Db      166 SPEDSDSDSD-EGEGLSPDEGDDSDSDDEETP-----TPKKPEAGKKRGAEN 219

```

```

QY      404 AVSMPI 409
Db      220 ALKTP 225

```

## RESULT 3

```

US-09-515-806-4
; Sequence 4, Application US/09515806
; Patent No. US20020132321A1
; GENERAL INFORMATION:
; APPLICANT: COOK, WILLIAM J.
; APPLICANT: KAPPELLER-LIBERMAN, ROSANA
; TITLE OF INVENTION: 14790. NOVEL PROTEIN KINASE MOLECULE AND USES THEREFOR
; FILE REFERENCE: 38155-2002.00
; CURRENT APPLICATION NUMBER: US/09/515,806
; CURRENT FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1648
; TYPE: PRT
; ORGANISM: Murine Species
; US-09-515-806-4

```

## Query Match

```

Best Local Similarity 5.0%; Score 115; DB 10; Length 1648;
Matches 54; Conservative 31; Mismatches 98; Indels 56; Gaps 11;

```

```

QY      195 DYVPSTIVSRNGAGITFSPALASGOYLITLK-----IGRAQALVLEVNDRLCKIGS 250
Db      558 DYETVYIPSNQLPASAFSETQKQFSRFLFEPEQLQKGFAYIKVQ----- 607
QY      251 QNLFPSKCMTEYOQOTGFOGHELYPIADTNT---RHADVDYRGYEDILQWNNLNRK 306
Db      608 --NKLDCGYAVKRIPIPNASRHFRIKGEVTLRLHENVIRY---NAM--IERHE 659
QY      307 NPSAP-DPRPDSVP--QETPAVTKKAEGRTPDASESEKKAPPEDEDDMOAASGENPAA 363
Db      660 RAVPCTPPDCTPOAODSPATCGKTSQDTIELGSVEAAAPPILSSSVSTSAERST 719
QY      364 L-----PEDEVEDPETHD-----DPNSDPDYNMPAVIPEEETKSSN 403
Db      720 TRFPYTGODSSDEDED-ERDGVFSQSFLPASDSDSIIIFNE-----DENKSGN 770

```

## RESULT 4

```

US-09-883-720-12
; Sequence 12, Application US/09883720
; Patent No. US20020022256A1
; GENERAL INFORMATION:
; APPLICANT: Baldwin, Donald A.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Crane, Virginia C.
; TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses
; FILE REFERENCE: 5718-44,
; CURRENT APPLICATION NUMBER: US/09/883,720
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/282,305
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Zea mays
; US-09-883-720-12

```

## Query Match

```

Best Local Similarity 4.9%; Score 112.5; DB 10; Length 305;
Matches 50; Conservative 43; Mismatches 80; Indels 43; Gaps 9;

```

```

QY      190 QMAVAVYVP-STIVSRNGAGITFSPALASGOYLITLKIGRAQALVLEVNDRLCKI 248
Db      50 QMAVAVYVP-STIVSRNGAGITFSPALASGOYLITLKIGRAQALVLEVNDRLCKI 248

```



[illegible]

RESULT 8  
US-09-73

```

; Sequence 67, Application US/09738973
; Patent No. US20020110563A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Reed, Steven G.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Fling, Steven P.
; APPLICANT: Mohamatch, Raodoh
; APPLICANT: Algate, Paul A.
; APPLICANT: Secrist, Heather
; APPLICANT: Indirlas, Carol Yoseph
; APPLICANT: Benson, Darin R.
; APPLICANT: Elliot, Mark
; APPLICANT: Mannion, Jane
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITILE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.475C9
; CURRENT APPLICATION NUMBER: US/09/738,973
; CURRENT FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 587
;
; SOFTWARE: FastSeq for Windows Version 3.0
;
; SEQ ID NO 67
; LENGTH: 764
;
; TYPE: PRF
;
; ORGANISM: Homo sapien
;
; US-09-738-973-67

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Query Match	4.5%;	Score 103.5;	DB 10;	Length 764;
Best Local Similarity	23.5%;	Pred. No. 0.81;		
Matches	48;	Conservative	30;	Mismatches 73;
				Indels 53;
				Gaps 9;

QY	230	RRACRALVYLEVN----	DRCLKIGSOLNLPJSCWTTEDYOTGFQGEHLYPIADTNRH	28
		: : : : :	: : : : :	
Db	577	KFSOELLNGEINLHPLKRWVEYIGSR-----	W-----GRISQSGREHYKLKAEQOQ	62
QY	285	ADDVYRGYEDILQWRNNL-----	RKKNNSADPRDPDYPQELPAVYTKA	32
		: : : : :	: : : : :	
Db	626	-----YKVLHDLIMVWSLSPDRAPAAKEYISMKRKSMTLKGPNKRS-----	SRTLLOSKS	67
QY	330	EGRTPDAAASSEKAPPEDESEDDMOAELS--	GENPALPED-----DEVPETEHDOPNS	38
		: : : : :	: : : : :	
Db	676	ESEDEDEDEDEDEDEDEEDENGDSSEDDGSSSSSEDESDGDENEDEDEDDDE	73	
QY	382	DPDYNDMPAVIPIVEETTKSSNAV	405	
Db	736	DDDEDEDNES-----EGSSSSSSSL	755	

RESULT 9  
US-09-765-272-90

Sequence 90, Application US/09765272  
Patent No. US20020061545A1  
GENERAL INFORMATION:  
APPLICANT: Choi et. al.  
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines  
NUMBER OF SEQUENCES: 452  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA

ZIP: 20850  
COMPUTER READABLE FORM:

```

? MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
? COMPUTER: HP Vectra 486/33
? OPERATING SYSTEM: MSDOS version 6.2
? SOFTWARE: ASCII Text

```

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/765,272  
FILING DATE: 22-Jan-2001  
CLASSIFICATION: G06F0007/00

CLASSIFICATION: <UNKNOWN>  
PRIOR APPLICATION DATA:

```

; APPLICATION NUMBER: 08/961,083
; FILING DATE: <Unknown>

```

ATTORNEY/AGENT INFORMATION:  
NAME: Brookes, A. Anders

REGISTRATION NUMBER: 36,373

REFERENCE/DOCUMENT NUMBER: PB340PZ  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-85  
TELEFAX: (301) 309-8512

```

; INFORMATION FOR SEQ ID NO: 90:
;
; SEQUENCE CHARACTERISTICS:

```

LENGTH: 258 amino acids  
TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: protein

```

;          SEQUENCE DESCRIPTION: SEQ ID NO: 90;
US-09-765-272-90

```

Query Match	.	4.5%;	Score 103;	DB 10;	Length 258;
Best local similarity		34.8%;	Prod No 0		

Best local similarity 24.0%, Freq. NO. 0.2;  
Matches 38; Conservative 24; Mismatches 51; Indels 40; Gaps 7;

276 PIADNTRHADVYRGIEDILQWNNLLRKKNPASADPRDPSVPOEIPAV--TKAEGRT 333

Db 94 PAESKVEOAGEPVAPRED-----EKAPVEPEKOPPE--DEEEKAVETTPKOEFST 142

334 PBAFSEFEKADDFDS-----EEDVOWACGDUATREDSUUES 1555

**EUDMCAEASGENPALPEDDEVEPE 3/2**

143 FDINAEIIVPEKKEI VNOSIEQKVEI PAVEKQTEPTTEPVEQAGE - PVAPREDEQAP - 200

QY 373 DLEHDDPNSDPDYNNDMPAVIVEETTKSSNAV 405  
| : : | : : :  
| : : | : : :

Db 201 -TAPVEPEKQPEVPEEKA---VEETPKPEDKI 229

## РЕЗУЛТАТИ 10

US-09-765-272-218

Sequence 218, Application US/09765272  
Patent No. US20020061545A1

```

; ; GENERAL INFORMATION:
; ;
; APPLICANT: Choi et. al.

```

TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccine  
NUMBER OF SEQUENCES: 452

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human genome Sciences, Inc.  
STREET: 9410 Key West Avenue

CITY: Rockville  
STATE: Maryland

COUNTRY: USA  
ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage  
COMPUTER: HP Vectra 486/33

```

OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text

```

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: ITS/09/765 373

DECLASSIFICATION AUTHORITY: 25X/03/1031212  
FILING DATE: 22-Jan-2001

CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/961,083

```

;
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
;   NAME: Brookes, A. Anders
;   REGISTRATION NUMBER: 36,373
;   REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (301) 309-8504
;   TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 218:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 565 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 218:
US-09-765-272-218

Query Match          4.5%; Score 103; DB 10; Length 565;
Best Local Similarity 24.8%; Pred. No. 0.59; Indels 40; Gaps 7;
Matches 38; Conservative 24; Mismatches 51;

QY 276 PIADNTRHADVDYRGYEDILQRMNNLLRKKNPSADPPRPSVPOEIPAV--TKKAGRT 333
   | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 98 PAGESKVEQAGEPYAPRED-----EKAPVEPEKQPEA-PEEKAVEETPKQEST 146
   | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
QY 334 PDASSSKKAPPEDS-----EDMQAASGENPALPEDDEVEPE 372
   | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 147 PDTRAEETVEPEKETVQSIQPKVETPAVEKQTEPEEPEKVEQAGE-PVAPFREDEQAP- 204
   | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
QY 373 DTEHDDPNSDPDYNDMPAVIPEETKSSNAV 405
   | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 205 -TAPVEPEKQPEVEPEEKA--VEETPKPEDKI 233

RESULT 11
US-09-759-508B-2
; Sequence 2, Application US/09759508B
; Publication No. US20020182599A1
; GENERAL INFORMATION:
; APPLICANT: Fishman, Mark C.
; TITLE OF INVENTION: Methods for Diagnosing and Treating Heart Disease
; FILE REFERENCE: 00786/381002
; CURRENT APPLICATION NUMBER: US/09/759,508B
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/175,787
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 26926
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-508B-2

Query Match          4.5%; Score 103; DB 9; Length 26926;
Best Local Similarity 32.1%; Pred. No. 1.3e+02; Indels 16; Gaps 3;
Matches 25; Conservative 12; Mismatches 25;

QY 305 KKNPSAPDPPDSVPQOEIFVTKKAGRTPDASSSEKKAP-----PESEDDMQAE----- 355
   | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 4536 KPPVEEPTPIAPVTVFVVGKAEKAPKEBAKPKGIVPKTKTSPTEARRKL 4595
   | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
QY 356 --ASGENPALPEDDEVP 371
   | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 4596 PGSGGEKP-----PDEAP 4608

RESULT 12
US-09-883-720-18
; Sequence 18, Application US/09883720
; Patent No. US20020022256A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Baldwin, Donald A.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Crane, Virginia C.
; TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses
; FILE REFERENCE: 5718-44,
; CURRENT APPLICATION NUMBER: US/09/883,720
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/282,305
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Zea mays
US-09-883-720-18

Query Match          4.4%; Score 101; DB 10; Length 285;
Best Local Similarity 22.0%; Pred. No. 0.34; Indels 42; Gaps 10;
Matches 46; Conservative 44; Mismatches 77;

QY 190 QMAVADVPSSTLYS-RNAGLITFSPTALSGOYLTLTKIGRAPQALVLEVNDRCLKI 248
   | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 2 EFNGEEVKGATVSCVKYGGDLVHLSQALG-----EKKASNAIVSVKIDDKLYL 54
   | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
QY 249 GSQNLFLPSKCWTTEQ-----YQFGQGHLPVADNTRHADVDYRGYEDILQRM 299
   | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 55 GT-----LSVEKRPQISCDLVFDKDFELSH-----NKTASVFEGCYKSPVPLF 98
   | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
QY 300 NNLLRKKNPSADPPRPSVP---QEIAPVTKKAGRT--PDASSSEKKAPPESEDDMQA 354
   | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 99 ES-DSGEDSDDEVEPDLIMONNEIKITAKVPVKVIGIONADETSGDDDDFTDSOS 157
   | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
QY 355 EASGENPALPEDDEVEPEDETE-HDDPNSD 382
   | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 158 EMSEDESS--DEDEVSSDTDTSDSGSE 184

RESULT 13
US-09-919-770-2
; Sequence 2, Application US/09919770
; Patent No. US20020048577A1
; GENERAL INFORMATION:
; APPLICANT: Bornstein, Paul
; APPLICANT: Kyriakides, Themis
; APPLICANT: Ratner, Buddy
; APPLICANT: Glachell, Cecilia
; APPLICANT: Martenson, Laura
; APPLICANT: Scatena, Marta
; TITLE OF INVENTION: Methods and Devices to Modulate the Wound Response
; FILE REFERENCE: US/09/919,770
; CURRENT APPLICATION NUMBER: US/09/919,770
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,071
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-919-770-2

Query Match          4.2%; Score 97.5; DB 10; Length 300;
Best Local Similarity 22.6%; Pred. No. 0.72; Indels 25; Gaps 5;
Matches 30; Conservative 19; Mismatches 59;

QY 278 ADNTRHADVDYRGYEDILQRMNNLLRKKNPSADPPDS---VPOEIPAVTKKAGRT 334
   | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 22 ADSGSSEKOLYNKYPDVAVTWLN-----PDPSQKONLLAPQTLPSKSNESHDDMD 72
   | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
QY 335 DASSSEKKAPPESEDDMQAASGENPALPEDDEVEPEDETHDDPNSD---PDYIYDMRA 391
   | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
```

Db 73 DMDDED----DDDHVDSQSDISNDSDVDVDTDDSHQSDSHHSEDESLVTDPEPTDLPA 128  
QY 392 -----VIVPEET 398  
Db 129 TEVFTPVVPTVDT 141

RESULT 14  
US-09-906-514-4  
; Sequence 4, Application US/09906514  
; Patent No. US20020170085A1  
; GENERAL INFORMATION:  
; APPLICANT: Kaeppler, Shawn  
; APPLICANT: Springer, Nathan  
; APPLICANT: Phillips, Ronald  
; TITLE OF INVENTION: Methyl Cpg Binding Domain Nucleic Acids from Maize  
; FILE REFERENCE: Methyblinding  
; CURRENT APPLICATION NUMBER: US/09/906,514  
; CURRENT FILING DATE: 2001-07-16  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 428  
; TYPE: PRT  
; ORGANISM: Zea mays  
US-09-906-514-4

Query Match 4.2%; Score 97; DB 9; Length 428;  
Best Local Similarity 28.9%; Pred. No. 1.3; Mismatches 47; Indels 18; Gaps 4;  
Matches 33; Conservative 16;

QY 310 APPPRDSVPOEIPAVTKKAEGTTPDAESSEKKAPPEDSED-----DMQAEASGE 359  
Db 239 APETKPDAPAAVPA--PAPENKPDAPAAAAPVDTKSVAPAAADAPDTKSVAPAA 295  
QY 360 NPAALPEDEDEVEDTDDHDPNSDPDYNDK-PAVIVPEET----TKSSNAVSMP 408  
Db 296 AAAPVPETKLVASADAVAAAPAPETKSDAPAAAPVETKPYAESADAVAAP 349

RESULT 15  
US-09-819-104A-5  
; Sequence 5, Application US/09819104A  
; Publication No. US20030027137A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, J. Don  
; TITLE OF INVENTION: NOVEL NUCLEAR RECEPTOR COREPRESSOR MOLECULES  
; FILE REFERENCE: IMG-030  
; CURRENT APPLICATION NUMBER: US/09/819,104A  
; CURRENT FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: 60/193,138  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 2462  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-819-104A-5

Query Match 4.1%; Score 95.5; DB 9; Length 2462;  
Best Local Similarity 21.4%; Pred. No. 20; Mismatches 61; Indels 57; Gaps 9;  
Matches 41; Conservative 33;

QY 236 LVTLVNDRCCLKIGSQLNLPKSCVTEOYOTGFOG--EH-----LYPIADTNRHAD 286  
Db 600 LASMENME-----SSRWTEEMETAKGLEHGRNWSAIAIMVGSKTVSQCK 646  
QY 287 DVYRGY-----EDILQRMNNLLRRKNPSAPPDRPDSVPOEIPAVTKKAEGTTPDAESSE 340  
Db 647 NFYFMYKKRONDELILQO-HRLKMEKERNA-----RRKKKKTTPAAASEE 689

QY 341 KKAPEDESDMQAASGENPALPPEDEVEDTEHDDPN-----SDPDYND-----MP 390  
Db 690 TAPPPAAEDBEMASGASANEELAEAEASQASGNEVPVGBCSGPAAVNNSSDTESVP 749  
QY 391 AVIPVEETTKSS 402  
Db 750 S--PREAETKDT 759

Search completed: February 19, 2003, 16:28:04  
Job time : 21 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 25, 2003, 12:53:18 ; Search time 2105 Seconds  
(without alignments)  
10040.432 Million cell updates/sec

Title: US-09-994-064-10

Perfect score: 1305  
Sequence: 1 ATGCACCGCTCCTATCTCAG.....TAAATGCGCGCTAGCTTA 1305

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_estba:\*  
3: em\_estba:\*  
4: em\_estba:\*  
5: em\_estba:\*  
6: em\_estba:\*  
7: em\_estba:\*  
8: em\_estba:\*  
9: em\_estba:\*  
10: em\_estba:\*  
11: em\_estba:\*  
12: em\_estba:\*  
13: em\_estba:\*  
14: em\_estba:\*  
15: em\_estba:\*  
16: em\_estba:\*  
17: em\_estba:\*  
18: em\_estba:\*  
19: em\_estba:\*  
20: em\_estba:\*  
21: em\_estba:\*  
22: em\_estba:\*  
23: em\_estba:\*  
24: em\_estba:\*  
25: em\_estba:\*  
26: em\_estba:\*  
27: em\_estba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41.4	3.2	958	17	CNS03PCF
2	41.2	3.2	669	12	BE776357
3	40.8	3.1	321	12	BG874723
4	40.8	3.1	529	17	AO876396
5	40.6	3.1	317	9	AA942788
6	40.2	3.1	212	9	AD012890

Result No.	Score	Query Match	Length	ID	Description
7	40.2	3.1	865	12	BG345158
8	40.0	3.1	688	12	BE521413
9	40.0	3.1	915	17	CNS0322R
10	40.0	3.1	1101	17	CNS000K2
11	40.0	3.1	1137	11	AY106791
12	39.6	3.0	558	12	BF825826
13	39.6	3.0	567	10	AV896003
14	39.6	3.0	596	14	BP007281
15	39.6	3.0	637	10	AV901789
16	39.6	3.0	660	14	BP002281
17	39.6	3.0	713	10	AV897918
18	39.6	3.0	715	10	AV892667
19	39.6	3.0	716	10	AV896867
20	39.6	3.0	1046	17	AG073741
21	39.4	3.0	451	9	AA552908
22	39.4	3.0	530	13	BM165497
23	39.4	3.0	633	13	BM177862
24	39.4	3.0	677	13	BM161314
25	39.4	3.0	709	14	BO840906
26	39.4	3.0	828	12	BG418286
27	39.2	3.0	1208	9	AL514927
28	39.2	3.0	533	9	AL828671
29	39.2	3.0	541	13	BI864958
30	39.2	3.0	577	9	AL721696
31	39.2	3.0	596	14	BO470238
32	38.8	3.0	567	10	BE393657
33	38.8	3.0	925	17	CNS0091P
34	38.6	3.0	364	9	AL723670
35	38.6	3.0	581	10	AV675337
36	38.4	2.9	295	12	BE799902
37	38.4	2.9	464	12	BE799902
38	38.4	2.9	2037	11	AY108662
39	38.2	2.9	317	10	AW281911
40	38.2	2.9	443	14	BM994532
41	38.2	2.9	450	13	BI366211
42	38.2	2.9	478	13	BI366327
43	38.2	2.9	485	9	AA202831
44	38.2	2.9	492	10	BE510710
45	38.2	2.9	508	13	BI229580

# ALIGNMENTS

RESULT 1  
CNS03PCF/c  
LOCUS  
DEFINITION  
Tetradon nigroviridis genome survey sequence PUC-ORI end of clone 044H14 of library G from Tetradon nigroviridis, genomic survey sequence.  
ACCESSION  
AL254472.1 GI:7975484  
VERSION  
GSS: genome survey sequence.  
KEYWORDS  
Tetradon nigroviridis.  
SOURCE  
Tetradon nigroviridis  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.  
REFERENCE  
1 (bases 1 to 958)  
Roest-Crollius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fitzames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissbach,J.  
Human gene number estimate provided by genome wide analysis using Tetradon nigroviridis DNA sequence  
Unpublished  
JOURNAL  
2 (bases 1 to 958)  
Roest-Crollius,H., Jallion,O., Dasilva,C., Fitzames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissbach,J.  
TITLE  
Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradon nigroviridis  
JOURNAL  
Unpublished





	Query Match	3.1%	Score 40.6;	DB 9,	Length 317;
	Berry Local Similarity	52.1%;	Pred. No.1.5;		
Matches	114; Conservative	0;	Mismatches 104;	Indels 1;	Gaps 1
QY	953 TCCCGCAAGAAATTCCTCCCCTGTACCCAAAGAACGGGAAGGGCGACCCTCCGAGCAGGAAA	1012			
Db	33 TCGCGCAACAACAGGCC-CCAGCTGAGCCCAAGCAATATAGCATGTCGCAGCCCGAAGAAGCAGAAA	92			
QY	1013 GCAGGAAAGAG-AG-GCCCCCTCCAAAGACTGGGAGACGACATGACAGCAGAGCTTCT	1071			
Db	93 CCCGCTGAGAGCGCCGCCGAGAGCAGAGGTAATGAGAGGGGGCTCAGAGGTTGGCAGAGATTGCA	152			
QY	1072 GGAGAAAAATCTGCCGCCCTCCGCCGAAGCAGCAGAACTCCCGAGAGACACGAGCAGAT	1131			
Db	153 GCACCCGGTGACAGTGCACCTACACCCGGGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT	212			
QY	1132 GATCCAAACTCGGATCTCGACTATTAACAATGATGAGCCC	1170			
Db	213 GCGCCCAAGCCCAACCTGACTTTATTCGAGAGACTTGGCCC	251			

RESULT 6	212 bp	mRNA	linear	EST 27-MAR-2000
AJ012890				
LOCUS				
DEFINITION	AJ012890			
ACCESSION	AF012890			
VERSION	AJ012890			
KEYWORDS	AJ012890.1	GI:7330436		
SOURCE	EST.			
ORGANISM	Entamoeba histolytica.			
REFERENCE	Entamoeba histolytica.			
AUTHORS	Eukaryota; Entamoebidae; Entamoeba.			
TITLE	1 (bases 1 to 212)			
JOURNAL	Willhoeft, U., Buss, H. and Tannich, E.			
MEDLINE	Analysis of cDNA expressed sequence tags from entamoeba			
COMMENT	histolytica: identification of two highly abundant polyadenylated			
FEATURES	transcripts with no overt open reading frames			
	Protein 150 (1), 61-70 (1999)			
	20187114			
	Contact: Tannich E			
	Bernhard Nocht Institute for Tropical Medicine			
	Bernhard Nocht Str. 74, 20359 Hamburg, Germany.			
	Location/Qualifiers			

[illegible]

RESULT 7	
BG345158	
LOCUS	BG345158
DEFINITION	865 bp mRNA, linear EST 22-OCT-2001 HVSMEG001801bf Hordeum vulgare pre-anthesis spike EST library

ACCESSION	HVCDNA0008 (white to yellow anther) Hordeum vulgare cDNA clone
VERSION	HVME00018018f, mRNA sequence.
KEYWORDS	BG345158
SOURCE	BG345158.2 GI:16318857
ORGANISM	EST. Hordeum vulgare. Hordeum vulgare.
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Hordeum.
AUTHORS	1 (bases 1 to 865) Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Fritch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Chol,D.W., Fenton,R.D., Close,S.J., Oates,R. and Maln,D. Development of a genetically and physically anchored EST resource for barley genomics: Morex pre-anthesis spike cDNA library Unpublished (2001) On Feb 27, 2001 this sequence version replaced gi:13157487.
JOURNAL	COMMENT
CONTACT	Wing RA Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288 Fax: 864 656 4293 Email: rwing@clemson.edu Seq primer: AATTACCTCCTCAAGGC High quality sequence stop: 856. Location/Qualifiers 1..865
FEATURES	
source	

```

FEATURES
Source
Location/Qualifiers
1. 865
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEG0018016f"
/clone_lib="Hordeum vulgare pre-anthesis spike EST library
HVCNDA0008 (white to yellow anther)"
/tissue_type="pre-anthesis spike"
/lab_host="SOLR"
/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI;
plants were grown in the greenhouse at the University of
California, Riverside (Fenton, SJ Close, TJ Close). Whole
spike with awns trimmed were collected at white, green and
yellow anther stages (Fenton). Total RNA was prepared from
each pool, equal quantities of all three RNA pools were
combined, poly(A) RNA was purified from the mixture, one
primary unamplified cDNA library was made, and 1 million
pfu were in vivo excised to give plasmidscript SK(-) cDNA
phagemids. These steps were performed in the TJ Close lab
(Choi) at the University of California, Riverside.
Phagemids were plated and picked at the Clemson University
Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins
and Wing) Plasmid DNA preparations, DNA sequencing and
sequence analysis were performed at CUGI (Wing, Yu, Frisch
, Henry, Simmons, Oates, Rambo, Main). The sequence has
been trimmed to remove vector sequence and contains a
minimum of 100 bases of phred value 20 or above. For more
details on library preparation and sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders
Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/gpapes/bgn/31/cover.html)"
196 a 217 c 271 g 181 t

```

Query March	3.1%	Score 40.2;	DB 12,	Length 865;
Best Local Similarity	53.5%	Pred. No. 3.6;		
Matches 84; Conservative	0;	Mismatches 73;	Indels 0;	Gaps 0
QY 1002	GGAGCGGAAGACGAGGAAAAGAGCCCTTCAGAAATCTCGAGGAGCGACATCGAGCG	1061		
Db 65	GGAGCGAAGCCGAGGAGCGCGCGGAGACGAAAGATTAACACGAGGAGCGACGCGAGCGA	124		

0Y	1063	AGAGGCTTCTGGAGAAATTCCTGCCGCCCTCCCGCAAGACGACGAATGCCGAGACAC	1121
Db	125	CGATGACGACGACGATGAGGATGATGACGACGACGACGACGACGACGACGACGACCA	184
0Y	1122	CGAGCAGCATGATCCAAACTCGATCTGACTGATATTAC	1158
Db	185	GGATCAGCAGGACGACCGCGCTACCGGAGACTGCTGC	221
RESULT 8			
LOCUS	BFS21413	688 bp	mRNA
DEFINITION	EST456889 DSIL Medicago truncatula cDNA clone pDSIL-4362, mRNA		
ACCESSION	BFS21413		
VERSION	BFS21413.1		
KEYWORDS	EST.		
SOURCE	barrel medic.		
ORGANISM	Medicago truncatula		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.		
REFERENCE	1 (bases 1 to 688)		
AUTHORS	Fedorova, M., Pearson, B.L., Samac, D.A., Vance, C.P., Gantt, G.S., Peng, H., Ellis, L., Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, L.E. and Fraser, C.M.		
TITLE	ESTs from leaves of Medicago truncatula after inoculation with Colletotrichum trifolii		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Deborah A. Samac Department of Plant Pathology University of Minnesota 495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA Tel: 612 625 1243 Fax: 651 649 5058 Email: debbys@uccn1.crl.umn.edu University of Minnesota name: M278858e TIGR sequence name: M7PDH37TK More information is available at: <a href="http://chrysle.tamu.edu/medicago">http://chrysle.tamu.edu/medicago</a> Seq primer: SKmod (CTA GAA CTA gfg GAT CC). Location/Qualifiers 1..688 /organism="Medicago truncatula" /cultivar="genotype A17" /db_xref="taxon:3880" /clone="pDSIL-4362" /clone_1fb="DSIL" /tissue_type="leaves infected with Colletotrichum trifolii" /dex_stage="cotyledons and primary leaves harvested 5 and 8 days after inoculation with Colletotrichum trifolii" /lab_host="E. coli strain XLOLR" /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA from cotyledons and primary leaves harvested 5 and 8 days after inoculation with Colletotrichum trifolii. The cDNA was directionally ligated into the uni-ZAP XR vector from Stratagene and packaged using GigaPack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in XLOLR cells. Note: EST may be of fungal origin."		
BASE COUNT	219 a	139 c	139 t
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Best Local Similarity	52.4%;	Pred. No. 3.6;	
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[illegible]



Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Joegenel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

**TITLE**  
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
**JOURNAL**  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
**MEDLINE**  
20202663  
**COMMENT**  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=MR2&t2=MR2-HN0036-171100-002-e036t3-2000-11-17&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 254.

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/db\_xref="taxon:9606"  
/clone\_lib="HN0036"  
/dev\_stage="Adult"  
/note="Organ: head normal; Vector: puc18; Site:1: Smal; Site:2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."  
BASE COUNT  
96 a 180 c 124 g 158 t  
ORIGIN

Query Match 3.0%; Score 39.6; DB 12; Length 558;  
Best Local Similarity 45.9%; Pred. No. 4.2;  
Matches 135; Conservative 0; Mismatches 159; Indels 0; Gaps 0;

QY 870 GGGATACGAAGATATTCGAGCGCTGGATATTTCTGAGCAAAAAGAACTCTAGCC 929  
DB 397 GGGACGCCAAGAGAGATTGGCTGTGTGAGCCCTTAAGACAAATAAGTCTCTGAG 338  
QY 930 GCCAGACCTCTGTCAGATCGTCCGCAAGAAATTCCTGTAACCAAGAAAGCGGA 989  
DB 337 TCCAAACATGTGCTGTGAAGCTGACCAAAAGAGCTGTCCAGACAGCTGTGAAGAGG 278  
QY 990 AGGGCCGACCCCGAGCAGCAAGAAAGCAAGAGCCCTCCAGAGACTCGGAGGA 1049  
DB 277 ACCCCAGTCCCTAGTAATCTCTCCGAGCAAGAGCCGCAAGCACTGGAGTGTA 218  
QY 1050 CGACATGCAAGCGCAGAGGCTTCTGAGAAATTCCTGCCCTCCCGAAGACGACGA 1109  
DB 217 GGAAGAGAGAGAGAAAGACTCTGAAGAAATGATGTAACACACGCGGAGCTTGGG 158  
QY 1110 CCCCCAGACACGACGATGATCCAACTCGAGTCTGACTATTACAATGA 1163  
DB 157 CTCGAGAGAGATGCTGATACGCTAGATGACTGAGCTGACTCCAACTCTGA 104

**RESULT 13**  
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**LOCUS**  
AV896003 Nori Satoh unpublished cDNA library, young adult Clona  
**DEFINITION**  
Intestinalis cDNA clone rclad43115 3', mRNA sequence.  
**ACCESSION**  
AV896003  
**VERSION**  
AV896003.1 GI:16885099  
**KEYWORDS**  
EST.  
**SOURCE**  
Clona intestinalis.

## ORGANISM

Clona intestinalis  
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
Phlebobranchia; Clonidae; Clona.

**REFERENCE**  
1 (bases 1 to 567)  
Sato, N., Satou, Y., Kohara, Y. and Shin-I, T.  
**TITLE**  
Expressed genes in Clona intestinalis  
**JOURNAL**  
Unpublished (2000)  
**COMMENT**  
Contact: Nori Satoh  
Department of Zoology  
Kyoto University  
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan  
Tel: 81-75-753-4081  
Fax: 81-75-705-1113  
Email: sato@ascidian.zool.kyoto-u.ac.jp.

**FEATURES**  
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/clone\_lib="rclad43115"  
/clone\_lib="Nori Satoh unpublished cDNA library, young adult"  
/tissue\_type="whole animal"  
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/note="Vector: pBluescript SK"

**BASE COUNT**  
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Query Match 3.0%; Score 39.6; DB 10; Length 567;  
Best Local Similarity 50.0%; Pred. No. 4.2;  
Matches 99; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 967 CCGCTTAACCAAGAAAGCGGAGGCGCACCCCGACCCAGAAAGCAGCAAGAG 1026  
DB 480 CCAACTGAAGAGTACTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 421  
QY 1027 GCCCTCCAGAGACCTCGAGAGAGATGACGAGGAGGCTCTGAGAAATTCCTGCC 1086  
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QY 1087 GCCCTCCAG 1146  
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QY 1147 CTTGACTATTACATGAC 1164  
DB 300 GAGCAGCAGCAGAGATGAC 283

**RESULT 14**  
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**LOCUS**  
BP007281 Nori Satoh unpublished cDNA library, young adult Clona  
**DEFINITION**  
Intestinalis cDNA clone clad43115 5', mRNA sequence.  
**ACCESSION**  
BP007281  
**VERSION**  
BP007281.1 GI:19498758  
**KEYWORDS**  
EST.  
**SOURCE**  
Clona intestinalis.  
**ORGANISM**  
Clona intestinalis.  
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
Phlebobranchia; Clonidae; Clona.

**REFERENCE**  
1 (bases 1 to 596)  
Sato, N., Satou, Y., Kohara, Y. and Shin-I, T.  
**TITLE**  
Expressed genes in Clona intestinalis  
**JOURNAL**  
Unpublished (2000)  
**COMMENT**  
Contact: Nori Satoh  
Department of Zoology  
Kyoto University  
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan  
Tel: 81-75-753-4081  
Fax: 81-75-705-1113  
Email: sato@ascidian.zool.kyoto-u.ac.jp.

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Location/Qualifiers

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Matches 99; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

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Db 319 CCAACTGAAAGATCTCTCGAGAGAGGAGACACAAAGGAGGAGGAGAGAA 378
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QY 1027 GCCCTTCAGAGACTCGAGAGACATGACAGGACAGAGGCTTCTGGAGAAATCCTGCC 1086
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Db 379 GAAGAGGAAAGACGATGATGATGACGACGATGACGACGATGATGATGATGATGATGAT 438
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QY 1087 GCCCTCCCGAAGACGACGAGTCCCGAGGACACGACGATGATCCAAACTCGGAT 1146
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Db 439 GACGAAGATATATGACGATGATGACGAGATGATGATGATGATGATGATGATGATGATGAT 498
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QY 1147 CTTGACTATTACATGAC 1164
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Db 499 GACGACGACGACGATGAC 516

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RESULT 15
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LOCUS          AV901789      Nori Satoh unpublished cDNA library, young adult Clona
DEFINITION     AV901789      intestinalis cDNA clone ciad52h17 3', mRNA sequence.
ACCESSION      AV901789.1      GI:16890887
VERSION        AV901789.1
KEYWORDS       EST.
SOURCE         Clona intestinalis.
ORGANISM       Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
                Phlebobranchia; Clonidae; Clona.
REFERENCE      1 (bases 1 to 637)
AUTHORS        Satoh, N., Satou, Y., Kohara, Y. and Shin-I, T.
TITLE          Expressed genes in Clona intestinalis
JOURNAL        Unpublished (2000)
COMMENT        Contact: Nori Satoh
                Department of Zoology
                Kyoto University
                Sakyo-Ku, Kyoto 606-8502, Japan
                Tel: 81-75-753-4081
                Fax: 81-75-705-1113
                Email: satoh@scidian.zool.kyoto-u.ac.jp.

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                /db_xref="taxon:7719"
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                /clone_lib="Nori Satoh unpublished cDNA library, young
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                /tissue_type="whole animal"
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BASE COUNT      165 a      161 c      93 g      218 t
ORIGIN

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Query Match      3.0%; Score 39.6; DB 10; Length 637;
Best Local Similarity 50.0%; Pred. No. 4.5;
Matches 99; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

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QY 967 CCCGCTGTACCAAGAAAGGCGGACACCCCGGACGACGAGAAAGACGAAAGAG 1026

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Db 575 CCAACTGAAAGATCTCTCGAGAGAGGAGACGACAAAGAGGAGGAGGAGAGAGAA 516
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QY 1027 GCCCTTCAGAGACTCGAGAGACATGACAGGACAGAGGCTTCTGGAGAAATCCTGCC 1086
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QY 1147 CTTGACTATTACATGAC 1164
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Db 395 GACGACGACGACGATGAC 378

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Search completed: February 25, 2003, 13:44:50
Job time : 2117 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 25, 2003, 13:06:38 ; Search time 63 Seconds  
(without alignments)  
6352.590 Million cell updates/sec

Title: US-09-994-064-10

Perfect score: 1305  
Sequence: 1 ATGCACCGCTCTCATCTCAG.....TAAATGCCGCTAGCTAA 1305

Scoring table:  
IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 862724

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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Issued Patents, NA: \*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1305	100.0	1305	2	US-08-484-575A-19
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4	1305	100.0	1305	3	US-08-486-414-19
5	1305	100.0	1305	5	PCT-US94-01826A-19
6	1305	100.0	1305	5	PCT-US94-02252A-19
7	1305	100.0	1305	5	PCT-US96-03916-10
8	1305	100.0	13473	5	PCT-US96-03916-10
9	1305	100.0	18912	5	PCT-US96-03916-59
10	44.4	3.4	7218	1	US-08-222-463-14
11	42	3.2	42	5	PCT-US96-03916-33
12	41.6	3.2	390	4	US-09-197-649-7
13	37.4	2.9	2277	1	US-08-676-967-2
14	37.4	2.9	2277	1	US-08-676-974-2
15	37.4	2.9	2277	2	US-09-098-487-2
16	36.2	2.8	1268	1	US-08-440-856A-9
17	36.2	2.8	2943	1	US-08-042-747A-7
18	35.4	2.7	3489	2	US-08-728-323A-1
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22	35.4	2.7	32207	4	US-09-230-371A-20
23	35.2	2.7	150	2	US-07-829-461A-8
24	34.8	2.7	1187	1	US-08-440-856A-2
25	34.6	2.7	1191	4	US-09-386-588A-1
26	34.4	2.6	68750	3	US-09-335-409-1
27	34.4	2.6	68750	4	US-09-568-102-1

28	34.4	2.6	68750	4	US-09-567-969-1	Sequence 1, Appl1
29	34.4	2.6	68750	4	US-09-568-480-1	Sequence 1, Appl1
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32	34.4	2.6	68750	4	US-09-567-899-1	Sequence 1, Appl1
33	34.2	2.6	799	4	US-08-998-416-420	Sequence 420, App
34	34.2	2.6	5063	1	US-08-185-432-1	Sequence 1, Appl1
35	33.4	2.6	1100	3	US-09-248-335-53	Sequence 3, Appl1
36	33.2	2.5	4403765	4	US-09-103-840A-2	Sequence 2, Appl1
37	32.8	2.5	2984	5	PCT-US93-00893-1	Sequence 1, Appl1
38	32.8	2.5	2984	5	PCT-US93-00893-2	Sequence 2, Appl1
39	32.8	2.5	3777	3	US-09-121-321-15	Sequence 15, Appl1
40	32.8	2.5	3777	4	US-08-933-803A-15	Sequence 15, Appl1
41	32.6	2.5	6305	4	US-09-221-017B-256	Sequence 256, App
42	32.4	2.5	1476	4	US-09-434-288-12	Sequence 12, Appl1
43	32.4	2.5	28804	2	US-08-592-874-1	Sequence 1, Appl1
44	32.4	2.5	28804	3	US-09-096-942-2	Sequence 2, Appl1
45	32.4	2.5	28804	3	US-09-096-867-2	Sequence 2, Appl1

#### ALIGNMENTS

RESULT 1  
US-08-484-575A-19  
Sequence 19, Application US/08484575A  
Patent No. 5925358  
GENERAL INFORMATION:  
APPLICANT: Mark D. Cochran and David E. Junker  
TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses Thereof  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: John P. White  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,575A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: White Esq, John P.  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)278-0450  
TELEFAX: (212)391-0525  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1305 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1305  
US-08-484-575A-19  
Query Match 100.0%; Score 1305; DB 2; Length 1305;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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OY 61 AAACATGATGATGGGTGGAAGAAAGGTCGTCAGGCGGACGTGTAATCACTCTTTC 120
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DB 1021 AAGAAAGCGCTTCAGAAAGTCTGAGAGCAGATGCGAGGAGGCTTCTGAGAAAT 1080
OY 1081 CCGGCCGCTCCCGCAAGACGAAAGTCCCGGAGGACACCGACGATGATCCAAAC 1140
DB 1081 CCGGCCGCTCCCGCAAGACGAAAGTCCCGGAGGACACCGACGATGATCCAAAC 1140

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OY 1141 TCGACTCTGACTATTAACATGACATGCGCGCGCTGATCCCGGTGAGAGAGACTATAA 1200
DB 1141 TCGACTCTGACTATTAACATGACATGCGCGCGCTGATCCCGGTGAGAGAGACTATAA 1200
OY 1201 AGTCTAATGCCGCTCCATCCCATATTCGCGCGCTTCTGATGCGCGCGCGCTC 1260
DB 1201 AGTCTAATGCCGCTCCATCCCATATTCGCGCGCTTCTGATGCGCGCGCGCTC 1260
OY 1261 GTGGGCTACTGTTTGGAGCATGTAATAATGCGCGCTAGCTAA 1305
DB 1261 GTGGGCTACTGTTTGGAGCATGTAATAATGCGCGCTAGCTAA 1305

RESULT 2
US-08-477-459-19
; Sequence 19, Application US/08477459
; Patent No. 6001369
; GENERAL INFORMATION:
; APPLICANT: Mark D. Cochran
; TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1305 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1305
; US-08-477-459-19

Query Match 100.0%; Score 1305; DB 3; Length 1305;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ATGACCGCTCTCATCTCAGACGGGACATCGGCTTACTACGGGAAAGAGAGTGTCTTAAC 60
DB 1 ATGACCGCTCTCATCTCAGACGGGACATCGGCTTACTACGGGAAAGAGAGTGTCTTAAC 60
OY 61 AAACATGATGATGGGTGGAAGAAAGGTCGTCAGGCGGACGTGTAATCACTCTTTC 120
DB 61 AAACATGATGATGGGTGGAAGAAAGGTCGTCAGGCGGACGTGTAATCACTCTTTC 120
OY 121 TGGACTTGTGTAGATTAATGCGGAGCATATCTCTTTGTAAGCAAGCGTAAGACCGC 180
DB 121 TGGACTTGTGTAGATTAATGCGGAGCATATCTCTTTGTAAGCAAGCGTAAGACCGC 180

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1021 AAGAGGCGCGCTCCAGAGACTCGGAGGAGACATGACAGGAGGCTTCTGAGAAAAT 1080  
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1081 CCGGCGCGCTCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140  
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1141 TCGGATCTGACTATTTACATGACATGCGCGCTGATCCCGGTGGAGGAGACTACTAAA 1200  
1201 AGTTCTAATGCGCTGCTCAGATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1260  
1201 AGTTCTAATGCGCTGCTCAGATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1260  
1261 GTGGGGCTACTGTTGGAGCATGCTAAATGCGCGGCTAGCTAA 1305

1261 GTGGGGCTACTGTTGGAGCATGCTAAATGCGCGGCTAGCTAA 1305  
RESULT 3  
US-08-479-869-19  
Sequence 19, Application US/08479869  
Patent No. 6123949  
GENERAL INFORMATION:  
APPLICANT: Cochran Ph.D, Mark D  
TITLE OF INVENTION: Recombinant Fowlpox Virus S-FPV-043 and  
TITLE OF INVENTION: Uses thereof  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
Zip: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/479,869  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/024,156  
FILING DATE: 26-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: White Esq, John P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)977-9550  
TELEFAX: (212)664-0525  
TELEX: 422523  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1305 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
MOLECULE TYPE: linear  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1305  
US-08-479-869-19  
Query Match 100.0%; Score 1305; DB 3; Length 1305;  
Best local Similarity 100.0%; Pred. No. 0;  
Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 301 ATACCGCGGTTGGCCCGGTATACAGATACCTCTAGGGTATACAGAGCGTGGACCTT 360  
Db 301 ATACCGCGGTTGGCCCGGTATACAGATACCTCTAGGGTATACAGAGCGTGGACCTT 360  
QY 361 GTCAGCTCAACCCGATTTCTAAGTGCAGCATGATATGCGGGGCGCAAGAAAGAG 420  
Db 361 GTCAGCTCAACCCGATTTCTAAGTGCAGCATGATATGCGGGGCGCAAGAAAGAG 420  
QY 421 AAGGGGGCCCTTTGAGGCGCTCCGCTGCTGTTCTACGTGATTAAGGCGAGCGGC 480  
Db 421 AAGGGGGCCCTTTGAGGCGCTCCGCTGCTGTTCTACGTGATTAAGGCGAGCGGC 480  
QY 481 GAGGACAGTACTGTCCAACTATAGAAAGAGTACAGGAAAGTGGCGAGTACAACTG 540  
Db 481 GAGGACAGTACTGTCCAACTATAGAAAGAGTACAGGAAAGTGGCGAGTACAACTG 540  
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Db 601 CTGTATCGGGAATGGCGCGGAGTACTATATCTCCCACTGCTGCTGCTGCGC 660  
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Db 661 CAATACTGCTGACCCCTGAATAATCGGGAGATTGGCGAAACAGCTCTCGTACAGACC 720  
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Db 721 GTTACAGATGCTGTTTAAAGATCGGGTGCAGCTTACTTTTACCGTGAAGTCTGG 780  
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Db 781 ACAACAGACAGTATCAGACTGATTTCAAGGGAACCTTATCCGATCGAGACACC 840  
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Db 841 AATACAGACAGCGGAGCAGATATCGGGGATACGAAGATATTTCTGAGCGCTGGAA 900  
QY 901 AATTGCTGAGGAAAGAAATCTTACGCGGCCAGACCTCTGTCAGATAGCGTCCGCAG 960  
Db 901 AATTGCTGAGGAAAGAAATCTTACGCGGCCAGACCTCTGTCAGATAGCGTCCGCAG 960  
QY 961 GAAATTCGCGTGTATCAAGAAAGGGAAGGCGCACCCCGGACGCAAGAAAGCGAA 1020  
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Db 1021 AAGAAAGCCCTTCAGAAAGTCTGAGGAGCAGATCAGAGGAGCTCTGAGAGAAAT 1080  
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Db 1081 CCGCGCGCCCTCCGAAAGCAGAGTCCCGGAGGAGACCCGAGCAGAAAGCGGAA 1140  
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Db 1141 TCGGATCTGACTATTTACATGACATGCCCGCTGATCCCGTGGAGAGACTACTAA 1200  
QY 1201 AATTCTAATGCGGTCCATGCGCAATATTCGCGGCTGATGAGCTGCGCGGTGCGCTC 1260  
Db 1201 AATTCTAATGCGGTCCATGCGCAATATTCGCGGCTGATGAGCTGCGCGGTGCGCTC 1260  
QY 1261 GTGGGGCTACTGTTGGGAGCATGTAATAATGCGCGGTAGCTAA 1305  
Db 1261 GTGGGGCTACTGTTGGGAGCATGTAATAATGCGCGGTAGCTAA 1305

RESULT 4

US-08-486-414-19  
; Sequence 19, Application US/08486414B  
; Patent No. 6136318  
; GENERAL INFORMATION:  
; APPLICANT: Cochran, Mark D.  
; APPLICANT: Junker, David E.  
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUSES AND USES THEREOF  
; FILE REFERENCE: 42771D  
; CURRENT APPLICATION NUMBER: US/08/486,414B  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 1305  
; TYPE: DNA  
; ORGANISM: Fowlpox virus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(432)  
US-08-486-414-19  
Query Match 100.0%; Score 1305; DB 3; Length 1305;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGCACCGCTGCATCTCAGAGGCACTGCGTTACTAGCGAAAGAGAGGTGCTTAAC 60  
Db 1 ATGCACCGCTGCATCTCAGAGGCACTGCGTTACTAGCGAAAGAGAGGTGCTTAAC 60  
QY 61 AAACACATGATTTGGGTTGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120  
Db 61 AAACACATGATTTGGGTTGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120  
QY 121 TCGACTTGTGTAGAGTATATGCGGAGCATATCTCTTGTACGCAAGCATATGAGACCG 180  
Db 121 TCGACTTGTGTAGAGTATATGCGGAGCATATCTCTTGTACGCAAGCATATGAGACCG 180  
QY 181 CATTATTTTGAAGATGCTTTTGGACTATGCTAGCTGCTTCTCTGCTGCTAGCCAG 240  
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Db 1021 AAGAAGCCCTCCAGAGACTCGGAGGAGCAGATGCGAGGAGGCTTCTGGAGAAAT 1080  
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Db 1081 CCTGCCGCTCCCGGAGAGAGAGAGTCCCGAGAGACACCGAGCAGATGATCCAAAC 1140  
QY 1141 TCGGATCTGATATTAATGATGACGCGCGCTGATCCCGGTGGAGAGACTACTAAA 1200  
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Db 1141 TCGGATCTGATATTAATGATGACGCGCGCTGATCCCGGTGGAGAGACTACTAAA 1200  
QY 1201 AGTTCTAATGCGCTCTCATGCCCCATATTCGCGGCGTTCTGAGCCTGCGCGCTC 1260  
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Db 1201 AGTTCTAATGCGCTCTCATGCCCCATATTCGCGGCGTTCTGAGCCTGCGCGCTC 1260  
QY 1261 GTGGGCTACTGTTTGAGAGATGTAATGCGCGCTGACTAA 1305  
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Db 1261 GTGGGCTACTGTTTGAGAGATGTAATGCGCGCTGACTAA 1305

RESULT 5  
PCT-US94-01826A-19  
; Sequence 19, Application PC/TUS9401826A  
; GENERAL INFORMATION:  
; APPLICANT: Syntro Corporation, et al.  
; TITLE OF INVENTION: Recombinant Fowlpox Virus S-FPV-043 and Uses Thereof  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: John P. White  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10112  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/01826A  
; FILING DATE: 28-FEB-1994  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White Esq. John P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)977-9550  
; TELEFAX: (212)664-0525  
; TELEX: 422523  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1305 base pairs

TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1305  
PCT-US94-01826A-19

Query Match 100.0%; Score 1305; DB 5; Length 1305;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACCGCTCTCATCTTCAGACGGCAGCTCGGCTTACTACGCGAAAGAGAGAGGCTTTAAC 60  
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Db 1 ATGACCGCTCTCATCTTCAGACGGGAGACTCGGCTTACTACGCGAAAGAGAGGAGGCTTTAAC 60  
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Db 61 AAACATATGATTTGCGTGAAAAACGCTGCTCAGGCGCAGCTGATTTACTCTTTTC 120  
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Db 121 TGGAATGTGTACAGGATATGCGGAGCATATCTGCTTTAGCGAACGCTATGAGCCGC 180  
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Db 361 GTGAGCTCAACCCGATTTCTACGCTGAGCAGCATGATATGCGGCGCCAAAGAAAAG 420  
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Db 421 AAGGGGGCCCTTTCGAGGCTCCGCTGCTGCTTCTACGTTTAAGGGGAGAGCGGC 480  
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Db 601 CTGTATCGGCAATATGGGCGGAGTGAATTTTCCCCACCTGCTGCGCTCTGCGC 660  
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Db 721 GTTACGATGCTGTTAAAGATGGGCGCAGCTTAACCTTTTACCGTCGAATGCGG 780  
QY 781 ACAACAGACAGTATCAGACTGATTTCAAGCGCAACCTTTTATCCGATGCGACACC 840  
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Db 781 ACAACAGACAGTATCAGACTGATTTCAAGCGCAACCTTTTATCCGATGCGACACC 840  
QY 841 AATACAGACAGCGGAGCAGATATTCGGGATACGAAGATATTCGACGCTGGAAT 900  
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Db 841 AATACGACACGCGGACGACGTATATCGGGGATACGAAGATATTCGACGGCTGAAT 900  
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QY 1021 AAGAAGGCGCCGTCGAGAGACTCGAGACGACATGCGAGGAGGCTTTCGAGAAAT 1080  
Db 1021 AAGAAGGCGCCGTCGAGAGACTCGAGAGACATGCGAGGAGGCTTTCGAGAAAT 1080  
QY 1081 CCGTCCGCGCTCCCGAAGACGAGAAAGTCCCGAGACACCGAGACGATGATCCAAAC 1140  
Db 1081 CCGTCCGCGCTCCCGAAGACGAGAAAGTCCCGAGACACCGAGACGATGATCCAAAC 1140  
QY 1141 TCGGATCTGACTATTAACATGACATGCGCGGCTGATCCCGGTGAGAGAGACTACTAAA 1200  
Db 1141 TCGGATCTGACTATTAACATGACATGCGCGGCTGATCCCGGTGAGAGAGACTACTAAA 1200  
QY 1201 AGTCTATGCGCGCTGCTCATGCTCCATATTCGCGGCGCTTCGATGCGGCTGCGGCTC 1260  
Db 1201 AGTCTATGCGCGCTGCTCATGCTCCATATTCGCGGCGCTTCGATGCGGCTGCGGCTC 1260  
QY 1261 GTGGGCTACTGTTTGGAGCAGTGAATGCGCGGCTAGCTTAA 1305  
Db 1261 GTGGGCTACTGTTTGGAGCAGTGAATGCGCGGCTAGCTTAA 1305

RESULT 6  
PCT-US94-02252A-19  
Sequence 19, Application PC/TUS9402252A  
APPLICANT: Syntro Corporation, et al.  
TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses Thereof  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/02252A  
FILING DATE: 28-FEB-1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: White Esq, John P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)977-9550  
TELEFAX: (212)664-0525  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1305 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1305  
PCT-US94-02252A-19.

Query Match 100.0%; Score 1305; DB 5; Length 1305;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACCGTCTCTCATCTCAGACGGCACTCGCTTACTACCGGAAAGAGGCTTTAAC 60  
Db 1 ATGACCGTCTCTCATCTCAGACGGCACTCGCTTACTACCGGAAAGAGGCTTTAAC 60  
QY 61 AAACACATGATGCGGTGAAAAAGGTGCTGCTCAGGCGCACCTGATTCACCTCTTTT 120  
Db 61 AAACACATGATGCGGTGAAAAAGGTGCTGCTCAGGCGCACCTGATTCACCTCTTTT 120  
QY 121 TGGACTGTGTGACAGATTAATGCGGAGCATATCTGCTTGTACGCAACGCTATGACCG 180  
Db 121 TGGACTGTGTGACAGATTAATGCGGAGCATATCTGCTTGTACGCAACGCTATGACCG 180  
QY 181 CATTATTTTGAAGAAATGCTTTTGGACTATGCTACTGCTTCTTCTGCTAGCCAG 240  
Db 181 CATTATTTTGAAGAAATGCTTTTGGACTATGCTACTGCTTCTTCTGCTAGCCAG 240  
QY 241 AGCAGCGCGCGCTCAGCTACGACTACATTTTAAAGCGCGCGCTCGACGCGTAAAC 300  
Db 241 AGCAGCGCGCGCTCAGCTACGACTACATTTTAAAGCGCGCGCTCGACGCGTAAAC 300  
QY 301 ATACCGGCGGTGCGCGGTATTAACATACATCTACTAGGATATCAGAGGCTGCGACT 360  
Db 301 ATACCGGCGGTGCGCGGTATTAACATACATCTACTAGGATATCAGAGGCTGCGACT 360  
QY 361 GTGAGCTCAACCCGATTTCTAAGCTGAGCAGATGATGCGGCGCAAAAGAAAGAG 420  
Db 361 GTGAGCTCAACCCGATTTCTAAGCTGAGCAGATGATGCGGCGCAAAAGAAAGAG 420  
QY 421 AAGGGGGCGCTTTCAGAGCTCCGCTGCTGCTTCTACGTATTAAGGCGACAGCGGC 480  
Db 421 AAGGGGGCGCTTTCAGAGCTCCGCTGCTGCTTCTACGTATTAAGGCGACAGCGGC 480  
QY 481 GAGGACAACTACTGTCATATAGAAAAGATGACAGGAAATGGCGAGCTACTAACG 540  
Db 481 GAGGACAACTACTGTCATATAGAAAAGATGACAGGAAATGGCGAGCTACTAACG 540  
QY 541 CTATCTGAATGCGCGCTTCAATCTGCACAGATGCGGAGTGGAGCTATGTTCTAGCAC 600  
Db 541 CTATCTGAATGCGCGCTTCAATCTGCACAGATGCGGAGTGGAGCTATGTTCTAGCAC 600  
QY 601 CTTGATGCGGAAATGGCGCGGAGTACTATATCTCCGACCTGCTGCTGCGC 660  
Db 601 CTTGATGCGGAAATGGCGCGGAGTACTATATCTCCGACCTGCTGCTGCGC 660  
QY 661 CAATCTGCTGACCTGCAAAATCGGAGATTTGGCAAAAGCTCTGTAACTGTAGAA 720  
Db 661 CAATCTGCTGACCTGCAAAATCGGAGATTTGGCAAAAGCTCTGTAACTGTAGAA 720  
QY 721 GTTAACGATGCTGTTTAAAGATCGGTCGACGCTTAACTTTTACCTGCAAAATGCTG 780  
Db 721 GTTAACGATGCTGTTTAAAGATCGGTCGACGCTTAACTTTTACCTGCAAAATGCTG 780  
QY 781 ACAACAGAAAGTATCAGACGATGATTAAGGCGCAACCTTTATCCGATGCGACACCC 840  
Db 781 ACAACAGAAAGTATCAGACGATGATTAAGGCGCAACCTTTATCCGATGCGACACCC 840  
QY 841 AATACGACACGCGGAGGAGCTATATGCGGATACGAAGATTTGCGACGCTGGAGAT 900  
Db 841 AATACGACACGCGGAGGAGCTATATGCGGATACGAAGATTTGCGACGCTGGAGAT 900  
QY 901 AATTGCTGAGGAAAAAATCTTAGCGCGCCAGACCTCTGTCAGATAGGCTCCGCAA 960  
Db 901 AATTGCTGAGGAAAAAATCTTAGCGCGCCAGACCTCTGTCAGATAGGCTCCGCAA 960  
QY 961 GAAATTCCTGCTGTAAACCAAGAAAGCGGAGGCGCACCCCGAGCGCAAGAGCGCAA 1020  
Db 961 GAAATTCCTGCTGTAAACCAAGAAAGCGGAGGCGCACCCCGAGCGCAAGAGCGCAA 1020

```

1  TITLE OF INVENTION:  RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS
2  TITLE OF INVENTION:  AND USES THEREOF
3  NUMBER OF SEQUENCES:  72
4  CORRESPONDENCE ADDRESS:
5  ADDRESSEE:  Cooper & Dunham LLP
6  STREET:  1185 Avenue of the Americas
7  CITY:  New York
8  STATE:  New York
9  COUNTRY:  U.S.A.
10 ZIP:  10036
11
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE:  Floppy disk
14 COMPUTER:  IBM PC compatible
15 OPERATING SYSTEM:  PC-DOS/MS-DOS
16 SOFTWARE:  PatentIn Release #1.25
17
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER:  PCT/US96/03916
20 FILING DATE:  23-MAR-1995
21 CLASSIFICATION:
22
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER:  US 08/126,597
25 FILING DATE:  24-SEP-1993
26
27 ATTORNEY/AGENT INFORMATION:
28 NAME:  White, John P.
29 REGISTRATION NUMBER:  28,678
30 REFERENCE/DOCKET NUMBER:  39116-A
31
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE:  (212) 278-0400
34 TELEFAX:  (212) 391-0525
35
36 INFORMATION FOR SEQ ID NO:  10:
37 SEQUENCE CHARACTERISTICS:
38     LENGTH:  1305 base pairs
39     TYPE:  nucleic acid
40     STRANDEDNESS:  single
41     TOPOLOGY:  linear
42     MOLECULE TYPE:  DNA (genomic)
43     HYPOTHETICAL:  NO
44     ANTI-SENSE:  NO
45
46 FEATURE:
47     NAME/KEY:  CDS
48     LOCATION:  1..1305
49
50 PCT-US96-03916-10
51
52 Query Match:  100.0%;  Score 1305;  DB 5;  Length 1305;
53 Best Local Similarity 100.0%;  Pred. No. 0;
54 Matches 1305;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0

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Oy	1	ATTACCGTCCCTCATCTCCACAGCGCACTCCGCTTACTACGGCAAGAGAGGTGCTTAC	60
Db	1	ATGCAACGCTCTCATCTCCACAGCGCACTCCGCTTACTACGGCAAGAGAGGTGCTTAC	60
Oy	61	AAACACATGATTCGCGGTGGAAAAAGGTGCTGCTCAGCGGCAAGCTGTATTCACCTTTTC	120
Db	61	AAACACATGATTCGCGGTGGAAAAAGGTGCTGCTCAGCGGCAAGCTGTATTCACCTTTTC	120
Oy	121	TGCACTGTGTGTCAGAGATTATGCGGGAGCATATCTGCTTTGTACGACGCTATGGACGC	180
Db	121	TGGACTGTGTGTCAGAGATTATGCGGGAGCATATCTGCTTTGTACGCAACCTATGGACGC	180
Oy	181	CATTATATTTTGGAGATTCGTTTTTGACATATGTACTCTTTCTCTCTGCTAGCCAG	240
Db	181	CATTATATTTTGGAGATTCGTTTTTGAGACTATGTACTCTGCTTTCTCTGCTAGCCAG	240
Oy	241	AGCACCGCCGCCGTACAGTACGATCAATTTTATGCGCGTGCAGCGCTGACGCGCTAAC	300
Db	241	AGCACCGCGCGCGTACAGTACGATCAATTTTATGCGCGTGCAGCGCTGACGCGCTAAC	300
Oy	301	ATACCGGCGGTGGCCCGGTATTAACAGATTACTACTAGGGTATCAAGAGCTGCGACCTT	360
Db	301	ATACCGGCGGTGGCCCGGTATTAACAGATTACTACTAGGGTATCAAGAGCTGCGACGTT	360
Oy	361	GTCAGGCTCAACCCGATTTTAACTGAGACATATATTCGGCGCCAAAGAAAAAG	420
Db	361	GTCAGGCTCAACCCGATTTTAACTGAGACATATATTCGGCGCCAAAGAAAAAG	420
Oy	421	AAGGGGGCCCTTTCGAGGCTCCGTCGTCGTGTTCTACGTGATTAAAGGCGACAGCGC	480
Db	421	AAGGGGGCCCTTTCGAGGCTCCGTCGTCGTGTTCTACGTGATTAAAGGCGACAGCGC	480
Oy	481	GAGACAAAGTACTCTCCAACTATAGAAAAAGATACAGGAATGAGGCACTACAACTG	540
Db	481	GAGACAAAGTACTCTCCAACTATAGAAAAAGATACAGGAATGAGGCACTACAACTG	540
Oy	541	CTATCTGAATCGCGCTTCAATCTGCACAGATGTGGCAGTGAATGTTCTATGACACC	600
Db	541	CTATCTGAATCGCGCTTCAATCTGCACAGATGTGGCAGTGAATGTTCTATGACACC	600
Oy	601	CTTGTATCGGGAATTGGCGGGGACGTGACTATTTTCCCCAGATGCTGCTGCTGAGC	660
Db	601	CTTGTATCGGGAATTGGCGGGGACGTGACTATATTTCCCCAGATGCTGCTGCTGAGC	660
Oy	661	CAATACTTGTGACCCCTGAATAATCGGGAGATTTGCGCAAAACGCTCTGTAACTTAGAA	720
Db	661	CAATACTTGTGACCCCTGAATAATCGGGAGATTTGCGCAAAACGCTCTGTAACTTAGAA	720
Oy	721	GTTAACGATGGCTTTTAAAGATCGGGTGCACACTTTTAACTTTTAACTTTTAACTTTT	780
Db	721	GTTAACGATGGCTTTTAAAGATCGGGTGCACACTTTTAACTTTTAACTTTTAACTTTT	780
Oy	781	ACACACAAACAGTATCGACTGTGATTTCAAGGGGACACCTTATCCGATCGCACAACCC	840
Db	781	ACACACAAACAGTATCGACTGTGATTTCAAGGGGACACCTTATCCGATCGCACAACCC	840
Oy	841	AATACAGACACGCGGACGAGCTATATCGGGGATACGAAGATATTTCTGCAGCGCTGAT	900
Db	841	AATACAGACACGCGGACGAGCTATATCGGGGATACGAAGATATTTCTGCAGCGCTGAT	900
Oy	901	AATTGGTAGGAAAAAAGATTCCTAGGGGCGACCCGTCCAGATATAGGCTCCCGGAA	960
Db	901	AATTGGTAGGAAAAAAGATTCCTAGGGGCGACCCGTCCAGATATAGGCTCCCGGAA	960
Oy	961	GAATTTCCGCTGTAAACCAAGAAAGGGAAGGCGCACCCCGGACGCAAGAAAGCAGCGAA	1020
Db	961	GAATTTCCGCTGTAAACCAAGAAAGGGAAGGCGCACCCCGGACGCAAGAAAGCAGCGAA	1020
Oy	1021	AAGAAGGCCCCCTCCAGAAAGCTCGGAGAGACATCTCAGGACAGAGCTTCTGGAGAAAT	1080
Db	1021	AAGAAGGCCCCCTCCAGAAAGCTCGGAGAGACATCTCAGGACAGAGCTTCTGGAGAAAT	1080

QY 1081 CTTGCCGCCCCCTCCCGAGACGACGAAGTCCCGGAGACACCGAGCAGCATGATCCAAAC 1140  
 Db 1081 CTTGCCGCCCCCTCCCGAGACGACGAAGTCCCGGAGACACCGAGCAGCATGATCCAAAC 1140  
 QY 1141 TCGGATCTGACTATTACATGACATGCGCCGCGGTGATCCGCTGAGAGACTACTAAA 1200  
 Db 1141 TCGGATCTGACTATTACATGACATGCGCCGCGGTGATCCGCTGAGAGACTACTAAA 1200  
 QY 1201 AGTTCTAATGCGCTCTCCATGCGCCATATTCGCGGCGTTCGTAGCTGCGGCGGTGCGGCTC 1260  
 Db 1201 AGTTCTAATGCGCTCTCCATGCGCCATATTCGCGGCGTTCGTAGCTGCGGCGGTGCGGCTC 1260  
 QY 1261 GNGGGGCTACTGTTGGAGCATGCTAAAGCGCGCTAGCTAA 1305  
 Db 1261 GNGGGGCTACTGTTGGAGCATGCTAAAGCGCGCTAGCTAA 1305

RESULT 8  
PCT-US96-03916-1

Sequence 1, Application PC/TUS9603916  
 GENERAL INFORMATION:

APPLICANT: Wild, Martha A.  
 APPLICANT: Cochran, Mark D.  
 TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS  
 TITLE OF INVENTION: AND USES THEREOF  
 NUMBER OF SEQUENCES: 72  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP  
 STREET: 1185 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10036

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US96/03916  
 FILING DATE: 23-MAR-1995  
 CLASSIFICATION:

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/126,597  
 FILING DATE: 24-SEP-1993  
 ATTORNEY/AGENT INFORMATION:

NAME: White, John P.  
 REGISTRATION NUMBER: 28,678  
 REFERENCE/DOCKET NUMBER: 39116-A  
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 391-0525  
 TELEFAX: (212) 278-0400  
 INFORMATION FOR SEQ. ID NO. 1:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 13473 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHETICAL: NO

FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1059..2489  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 2575..4107  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 4113..4445  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 4609..5487

NAME/KEY: CDS  
 LOCATION: 5697..8654  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 9874..10962  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 11159..12658  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 12665..13447  
 PCT-US96-03916-1

Query Match 100.0%; Score 1305; DB 5; Length 13473;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACCGCTCCATCTCAGAGGCGACCTGCGCTTACTACGCGGAAGAGAGTGCTTAAC 60  
 Db 8462 ATGACCGCTCCATCTCAGAGGCGACCTGCGCTTACTACGCGGAAGAGAGTGCTTAAC 8521  
 QY 61 AAACACATGATGCGGTGGAACCGGTGCTGACGGCAGCTGATTCACCTTTTC 120  
 Db 8522 AAACACATGATGCGGTGGAACCGGTGCTGACGGCAGCTGATTCACCTTTTC 8581  
 QY 121 TGGACTTGTGTACGATTTATGCGGAGCATATCTGTTGTACGCAACGCTATGAGCCGC 180  
 Db 8582 TGGACTTGTGTACGATTTATGCGGAGCATATCTGTTGTACGCAACGCTATGAGCCGC 8641  
 QY 181 CATTTATTTTGGAGAACTTTTGGACTATGCACTGCTTTCTTCTGCTAGCCAG 240  
 Db 8642 CATTTATTTTGGAGAACTTTTGGACTATGCACTGCTTTCTTCTGCTAGCCAG 8701  
 QY 241 AGCACCGCGCGGTACAGTACATTTTATGAGCGGTGCGCGCTGACGCGCTAAC 300  
 Db 8702 AGCACCGCGCGGTACAGTACATTTTATGAGCGGTGCGCGCTGACGCGCTAAC 8761  
 QY 301 ATACCGGGGCTGGCGCGGTATACAGATACCTACCTAGGATATCAAGAGCTGCGAGCTT 360  
 Db 8762 ATACCGGGGCTGGCGCGGTATACAGATACCTACCTAGGATATCAAGAGCTGCGAGCTT 8821  
 QY 361 GTGAGCTCAACCCGATTTCTAACCTGAGCAGCATATGCGGCGCAAGAAAGAG 420  
 Db 8822 GTGAGCTCAACCCGATTTCTAACCTGAGCAGCATATGCGGCGCAAGAAAGAG 8881  
 QY 421 AAGGGGGCGCTTGGAGGCTCCGCTGCTGTTCTACGATTAAGGGGCGAGCGGC 480  
 Db 8882 AAGGGGGCGCTTGGAGGCTCCGCTGCTGTTCTACGATTAAGGGGCGAGCGGC 8941  
 QY 481 GAGGACAGTACTGTCATCTATAGAAAGATACAGAGGAATGGGCGAGCTCAACTG 540  
 Db 8942 GAGGACAGTACTGTCATCTATAGAAAGATACAGAGGAATGGGCGAGCTCAACTG 9001  
 QY 541 CTATCTGAATGCGCGCTTCAATCTGACAGATGCGGAGTGAATGTTCTTACGACC 600  
 Db 9002 CTATCTGAATGCGCGCTTCAATCTGACAGATGCGGAGTGAATGTTCTTACGACC 9061  
 QY 601 CTGTATGCGCAATGCGGCGGAGCTGACTATATCCCGCACTGCTGGCTCTGGC 660  
 Db 9062 CTGTATGCGCAATGCGGCGGAGCTGACTATATCCCGCACTGCTGGCTCTGGC 9121  
 QY 661 CAATACCTTGTGACCTGAAATGCGGAGATTTGCGCAACAGCTCTGTAACCTAGAA 720  
 Db 9122 CAATACCTTGTGACCTGAAATGCGGAGATTTGCGCAACAGCTCTGTAACCTAGAA 9181  
 QY 721 GTTAAGCATGCGGTGTTAAGATGCGGCTGCGAGCTTATCTTTTACCGTGAATGCTGG 780  
 Db 9182 GTTAAGCATGCGGTGTTAAGATGCGGCTGCGAGCTTATCTTTTACCGTGAATGCTGG 9241  
 QY 781 ACAACAGACAGTATGAGCTGATTTCAAGGGGAGACACTTATCCGATCGAGACACC 840  
 Db 9242 ACAACAGACAGTATGAGCTGATTTCAAGGGGAGACACTTATCCGATCGAGACACC 9301



QY	841	AATACAGACACGGGAGCGACGATATATTCGGGGATACGAAGATATTCGTGAGGCGTGGAAT	900
Db	9302	AATACAGACACGGGAGCGACGATATTCGGGGATACGAAGATATTCGTGAGGCGTGGAAT	9361
QY	901	AATTTGCTGAGAAAAAAGATTCCTACGGCCGACCCCTGCTCCAGATAGCCCTCCCGCA	960
Db	9362	AATTTGCTGAGAAAAAAGATTCCTACGGCCGACCCCTGCTCCAGATAGCCCTCCCGCA	9421
QY	961	GAATTTCCCGCTGTATACCAAGAAAGCGGAAGGCGCACCCCGAGCGCAGAAAGCGCA	1020
Db	9422	GAATTTCCCGCTGTATACCAAGAAAGGGAAGGCGCACCCCGAGCGCAGAAAGCGCA	9483
QY	1021	AAGAGGCGCCCTCGAAGAGCTCGAGAGACATCAGCAGAGGCTTCTGGAGAAAT	1080
Db	9482	AAGAGGCGCCCTCGAAGAGCTCGAGAGACATCAGCAGAGGCTTCTGGAGAAAT	9541
QY	1081	CTGCGCCGCTCCCCGAGACGACGAATGCCCGAGGACACCGAGCAGATGATCAAC	1140
Db	9542	CTGCGCCGCTCCCCGAGAGCGACGAATGCCCGAGGACACCGAGCAGATGATCAAC	9603
QY	1141	TCGATCTCACTATTACATGACATGCGCCGCGTATCCGCGTGGAGAGACTACTAA	1200
Db	9602	TCGATCTCACTATTACATGACATGCGCCGCGTATCCGCGTGGAGAGACTACTAA	9661
QY	1201	AGTTCTAATCGCTTCACATGCCATATTCGCGGCGCTTGTATGACCTGCGCGGCTCCGCTC	1260
Db	9662	AGTTCTAATCGCTTCACATGCCATATTCGCGGCGCTTGTATGACCTGCGCGGCTCCGCTC	9721
QY	1261	GTGGGCTACTGTTTGGAGACATCTGTAATAATGCGCGGTAGACTAA	1305
Db	9722	GTGGGCTACTGTTTGGAGACATCTGTAATAATGCGCGGTAGACTAA	9766

RESULT 9  
 PCT-US96-03916-59  
 Sequence 59, Application PC/TUS9603916  
 GENERAL INFORMATION:  
 APPLICANT: Wild, Martha A.  
 APPLICANT: Cochran, Mark D.  
 TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNOTRACHEITIS VIRUS  
 TITLE OF INVENTION: AND USES THEREOF  
 NUMBER OF SEQUENCES: 72  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Cooper & Dunham LLP  
 STREET: 1185 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10036  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US96/03916  
 FILING DATE: 23-MAR-1995  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/126,597  
 FILING DATE: 24-SEP-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: White, John P.  
 REGISTRATION NUMBER: 28,678  
 REFERENCE/DOCKET NUMBER: 39116-A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 278-0400  
 TELEFAX: (212) 391-0525  
 INFORMATION FOR SEQ ID NO: 59:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 18912 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single

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?      TOPOLOGY: linear
?      MOLECULE TYPE: DNA (genomic)
?      HYPOTHETICAL: N
?      ANTI-SENSE: N
?      FEATURE:
?      NAME/KEY: CDS
?      LOCATION: 697..1533
?      OTHER INFORMATION:
?      FEATURE:
?      NAME/KEY: CDS
?      LOCATION: complement (1900..2784)
?      OTHER INFORMATION:
?      FEATURE:
?      NAME/KEY: CDS
?      LOCATION: complement (2916..3605)
?      OTHER INFORMATION:
?      FEATURE:
?      NAME/KEY: CDS
?      LOCATION: 3694..5124
?      OTHER INFORMATION:
?      FEATURE:
?      NAME/KEY: CDS
?      LOCATION: 5210..7081
?      OTHER INFORMATION:
?      FEATURE:
?      NAME/KEY: CDS
?      LOCATION: 7245..8123
?      OTHER INFORMATION:
?      FEATURE:
?      NAME/KEY: CDS
?      LOCATION: 8333..11290
?      OTHER INFORMATION:
?      FEATURE:
?      NAME/KEY: CDS
?      LOCATION: 11098..12402
?      OTHER INFORMATION:
?      FEATURE:
?      NAME/KEY: CDS
?      LOCATION: 12510..13598
?      OTHER INFORMATION:
?      FEATURE:
?      NAME/KEY: CDS
?      LOCATION: 13792..15291
?      OTHER INFORMATION:
?      FEATURE:
?      NAME/KEY: CDS
?      LOCATION: 15298..16080
?      OTHER INFORMATION:
?      FEATURE:
?      NAME/KEY: CDS
?      LOCATION: 16129..17013
?      OTHER INFORMATION:
?      FEATURE:
?      NAME/KEY: CDS
?      LOCATION: complement (17380..18216)
?      OTHER INFORMATION:
PCT-US96-03916-59
Query Match      100.0%; Score 1305; DB 5; Length 18912;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0.0;
Oy      1      ATGCACCGTCCTCATCTCTAGACGGCAGCTCGCTTACTACGCGAAGAGAGAGGTGCTTAAC 60
Db 11098 ATGCACCGTCTCCATCTCTAGACGGCAGCTCGCTTACTACGCGAAGAGAGAGGTGCTTAAC 11157
Oy      61      AAACACATGAGATTGGCGGTGGAAAAAGCGTGCTGCTCAGGGCGCAGCTGTATTCACTCTTTTC 120
Db 11158 AAACACATGAGATTGGCGGTGGAAAAAGCGTGCTGCTCAGGGCGCAGCTGTATTCACTCTTTTC 11217
Oy      121     TGGACTTGTGTGAGGATTATGCGGGAGCATATCTGCTTTGTATCGCAACCGCTATGACCGC 180
Db 11218 TGGACTTGTGTGAGGATTATGCGGGAGCATATCTGCTTTGTATCGCAACCGCTATGACCGC 11277

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QY 1261 GTGGGGCTACTGCTTTGGAGCATCGTAAATGCGCGCTAGCTAA 1305  
|||||  
Db 12358 GTGGGGCTACTGCTTTGGAGCATCGTAAATGCGCGCTAGCTAA 12402

```

RESULT 10
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOAMPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMUG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ. ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F15
; US-08-232-463-14

Query Match 3.4%; Score 44.4; DB 1; Length 7218;
Best Local Similarity 6.6%; Pred. No. 0.0015;
Matches 24; Conservative 186; Mismatches 152; Indels 0; Gaps 0;

0Y 718 GAAGTAAAGATCGCTGTTAAAGATCGGGTGCAGCTTAACCTTTTAAACCGTCGAATGC 777
Db 1483 GTAATTAAGTATCTATGCAAGTAGTAAGATGAGAAATTTGGTACRRRRRRRRR 1424
0Y 778 TGACACAAGACAGATATGACATGGAATTTCGAAGCGAACACCTTTATCCGATCCGACAC 837
Db 1423 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1364
0Y 838 ACCATACACGACGACGCGACGACGACTATATCGGGATACGAAGATATTTCTGCGCGCTGG 897
Db 1363 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1304
0Y 898 AATATTTGCTGAGAAAAAGAAATCTAGCGCGCAGACCTCGTCCGATAGAGCTCCG 957

```

QY	958	CAGAAATTCGCGTGAACCAAGAAAGGGAAGGCGACCCGGAGCGAGAAAGCAGC	1017
Db	1243	RR	1184
QY	1018	GAAAGAGAGGCCCTCAGAGACCTCGGAGACATCAGGAGAGGCTTCGGAGA	1077
Db	1183	RR	1124
QY	1078	AA 1079	
Db	1123	RR 1122	

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RESULT 11
PCT-US96-03916-33
; Sequence 33, Application PC/TUS9603916
; GENERAL INFORMATION:
; APPLICANT: Wild, Martha A.
; APPLICANT: Cochran, Mark D.
; TITLE OF INVENTION: RECOMBINANT INFECTIOUS LAYNOTRACHEITIS VIRUS
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/03916
; FILING DATE: 23-MAR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,597
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 39116-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; PCT-US96-03916-33

Query Match 3.2%; Score 42; DB 5; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.00067;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 695 CGCAACAGCTCTGTACTAGACGTTACGATCGCTGTT 736
Db 1 CGCAACAGCTCTGTACTAGACGTTACGATCGCTGTT 42

RESULT 12
US-09-197-649-7
Sequence 7, Application US/09197649
Patent No. 6194550

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GENERAL INFORMATION:
APPLICANT: Gold, Larry
APPLICANT: Tuerk, Craig
APPLICANT: Pribnow, David
APPLICANT: Smith, Jonathan D.
TITLE OF INVENTION: Systematic Polypeptide Evolution by Reverse Translation
FILE REFERENCE: NEX02/C1-CON
CURRENT APPLICATION NUMBER: US/09/197,649
CURRENT FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: 07/829,461
EARLIER FILING DATE: 1992-01-31
EARLIER APPLICATION NUMBER: 07/739,055
EARLIER FILING DATE: 1991-08-01
EARLIER APPLICATION NUMBER: 07/561,968
EARLIER FILING DATE: 1990-08-02
NUMBER OF SEQ. ID NOS: 26
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 390
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Sequence
OTHER INFORMATION: having a 120 repeat of AGC flanked by fixed
OTHER INFORMATION: fragments having NcoI restriction sites.
US-09-197-649-7

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Query Match	3.28;	Score 41.6;	DB 4;	Length 390;
Best Local Similarity	51.68;	Pred. No. 0.0026;		
Matches	95;	Conservative	0;	Mismatches 89;
			Indels	0;
			Gaps	0;

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Db	261	GACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC	320
QY	1123	GAGCAGCATATCCAACTGGATCTGACTATTTCATATGACATGACATGCCCGCTGATCCCG	1182
Db	321	GACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC	380
QY	1183	GTGG	1186
Db	381	ATGG	384

RESULT 13  
 US-08/676-967-2  
 Sequence 2, Application US/08676967  
 Patent No. 5747317  
 GENERAL INFORMATION:  
 APPLICANT: COLLINS, KATHLEEN  
 TITLE OF INVENTION: Human Telomerase  
 NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Science & Technology Law Group  
 STREET: 268 Bush Street, Suite 3200  
 CITY: San Francisco  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94104  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/676,967  
 FILING DATE:  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:



Db 647 ARMSNGTVAARARARGNNGNNGARGARGAYATGARGARGARAAYGAYG 706  
QY 1079 ATCTGCCGCCCTCCCGAGACGACGAGTCCCGAGGACACCGAGATGATCCAA 1138  
Db 707 AYGAYGAYGAYGAYGARGARGAGGNGTNTTYGAYGARGAYGARGARGARGARA 766  
QY 1139 ACTCGGA 1145  
Db 767 AYATHGA 773

Search completed: February 25, 2003, 14:51:28  
Job time : 114 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 25, 2003, 13:44:53 ; Search time 89 Seconds  
(without alignments)  
8235.274 Million cell updates/sec

Title: US-09-994-064-10

Perfect score: 1305  
Sequence: 1 ATGCACCGCCCTCATCTCAG.....TAAATGCCGCGTACTTAA 1305

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 442118 seqs, 280819700 residues

Total number of hits satisfying chosen parameters: 884236

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications -NA:\*  
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3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	1305	100.0	3605	10 US-09-881-457A-3	Sequence 3, Appl1
2	41.6	3.2	390	10 US-09-790-399-7	Sequence 7, Appl1
3	34.6	2.7	863	10 US-09-974-300-5249	Sequence 5249, Ap
4	34.6	2.7	1191	10 US-09-842-987-1	Sequence 1, Appl1
5	34.4	2.6	68750	9 US-10-014-717-1	Sequence 1, Appl1
6	34.2	2.6	384	10 US-09-864-761-24106	Sequence 24106, A
7	34.2	2.6	455	10 US-09-864-761-25125	Sequence 7383, Ap
8	34.2	2.6	563	10 US-09-864-761-7383	Sequence 8395, Ap
9	34.2	2.6	586	10 US-09-864-761-8395	Sequence 8395, Ap
10	34.2	2.6	2481	10 US-09-894-998-35	Sequence 35, Appl1
11	34	2.6	1038	10 US-09-974-300-2209	Sequence 2209, Ap
12	33.6	2.6	438	9 US-09-938-842A-125	Sequence 125, App
13	33.6	2.6	678	10 US-09-770-149-358	Sequence 358, App
14	33.6	2.6	1503	9 US-09-938-842A-1892	Sequence 1892, Ap
15	33.2	2.5	7386	9 US-09-819-104A-6	Sequence 6, Appl1
16	33.2	2.5	8544	9 US-09-819-104A-4	Sequence 4, Appl1
17	32.6	2.5	672	10 US-09-833-381-697	Sequence 697, App
18	32.6	2.5	2349	12 US-10-087-110-5	Sequence 5, Appl1
19	32.6	2.5	2663	12 US-10-087-110-1	Sequence 1, Appl1

20	32	2.5	4257	9 US-09-825-288A-1	Sequence 1, Appl1
C 21	31.8	2.4	414	10 US-09-983-965-338	Sequence 338, App
C 22	31.8	2.4	1020	9 US-09-738-626-2136	Sequence 2136, Ap
C 23	31.8	2.4	1359	9 US-09-738-626-2135	Sequence 2135, Ap
C 24	31.8	2.4	1473	9 US-09-995-898A-3	Sequence 3, Appl1
C 25	31.8	2.4	1560	9 US-09-995-898A-28	Sequence 28, Appl1
C 26	31.8	2.4	1624	10 US-09-795-380-19	Sequence 19, Appl1
C 27	31.8	2.4	2898	10 US-09-834-975-868	Sequence 868, App
C 28	31.8	2.4	2898	10 US-09-834-975-868	Sequence 868, App
C 29	31.8	2.4	3309400	9 US-09-738-626-1	Sequence 1, Appl1
C 30	31.6	2.4	705	9 US-09-285-306-68	Sequence 68, Appl1
C 31	31.4	2.4	1234	10 US-09-925-502-1	Sequence 752, App
C 32	31.4	2.4	1485	10 US-09-925-300-752	Sequence 993, App
C 33	31.4	2.4	1560	9 US-09-738-626-993	Sequence 3, Appl1
C 34	31.4	2.4	1864	10 US-09-770-621-3	Sequence 349, App
C 35	31.4	2.4	2135	10 US-09-925-297-349	Sequence 3, Appl1
C 36	31.4	2.4	2145	10 US-09-925-502-3	Sequence 3340, Ap
C 37	31.4	2.4	2856	9 US-09-738-626-3340	Sequence 1943, Ap
C 38	31.4	2.4	19334	10 US-09-764-865-1943	Sequence 1, Appl1
C 39	31.4	2.4	3309400	9 US-09-738-626-1	Sequence 1, Appl1
C 40	31.2	2.4	2820	10 US-09-924-858A-4	Sequence 4, Appl1
C 41	31.2	2.4	7367	9 US-10-024-632-7	Sequence 7, Appl1
C 42	31.2	2.4	13842	9 US-09-860-846-30	Sequence 30, Appl1
C 43	31.2	2.4	13842	10 US-09-861-289-30	Sequence 30, Appl1
C 44	31.2	2.4	36778	9 US-09-860-846-5	Sequence 5, Appl1
C 45	31.2	2.4	36778	10 US-09-861-289-5	Sequence 5, Appl1

#### ALIGNMENTS

RESULT 1  
US-09-881-457A-3  
; Sequence 3, Application US/09881457A  
; Patent No. US20020081316A1  
; GENERAL INFORMATION:  
; APPLICANT: Cochran, Mark D  
; APPLICANT: Cook, Stephanie M  
; TITLE OF INVENTION: NO. US20020081316A1 Avian Herpes Virus and Uses Thereof  
; FILE REFERENCE: SY01105110K  
; CURRENT APPLICATION NUMBER: US/09/881,457A  
; CURRENT FILING DATE: 2001-06-14  
; PRIOR APPLICATION NUMBER: 09/426,352  
; PRIOR FILING DATE: 1999-10-25  
; PRIOR APPLICATION NUMBER: 08/804,372  
; PRIOR FILING DATE: 1997-02-21  
; PRIOR APPLICATION NUMBER: PCT/US95/10245  
; PRIOR FILING DATE: 1995-08-09  
; PRIOR APPLICATION NUMBER: 08/663,566  
; PRIOR FILING DATE: 1996-06-13  
; PRIOR APPLICATION NUMBER: 08/288,065  
; PRIOR FILING DATE: 1994-08-09  
; PRIOR APPLICATION NUMBER: PCT/US93/05681  
; PRIOR FILING DATE: 1993-06-14  
; PRIOR APPLICATION NUMBER: 08/023,610  
; PRIOR FILING DATE: 1993-02-26  
; PRIOR APPLICATION NUMBER: 07/898,087  
; PRIOR FILING DATE: 1992-06-12  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: Patent Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 3605  
; TYPE: DNA  
; ORGANISM: Infectious Laryngotracheitis Virus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (585)..(1889)  
; OTHER INFORMATION: ILTV glycoprotein D  
; NAME/KEY: CDS  
; LOCATION: (1977)..(3085)  
; OTHER INFORMATION: ILTV glycoprotein I  
; US-09-881-457A-3

Query Match 100.0%; Score 1305; DB 10; Length 3605;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 585 ATGACCGTCTCTATCTCAGACGCGACTCGGCTTACTACGCGAAAGAGAGAGTGTCTTAC 644
QY 61 AACACATGATGATGCGGTGGAAAAAGGTCGTCAGGCGCGAGTGTATTCACCTTTTC 120
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DB 645 AAACACATGATGATGCGGTGGAAAAAGGTCGTCAGGCGCGAGTGTATTCACCTTTTC 704
QY 121 TGGACCTGTGTACAGATTATCGGGAGCATATCTGCTTTGTAGCAACGCTATGAGCCG 180
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DB 705 TGGACCTGTGTACAGATTATCGGGAGCATATCTGCTTTGTAGCAACGCTATGAGCCG 764
QY 181 CATTTATTTTGGAGAAATGCTTTTGGAGTATGCTATGCTTTCTTCTGCTAGCCAG 240
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DB 765 CATTTATTTTGGAGAAATGCTTTTGGAGTATGCTATGCTTTCTTCTGCTAGCCAG 824
QY 241 AGCACCGCGCGCTGACGTACGACTATTATAGCGCGCGCGCTGCGACGCGCTAAC 300
    |||
DB 825 AGCACCGCGCGCTGACGTACGACTATTATAGCGCGCGCGCTGCGACGCGCTAAC 884
QY 301 ATAACCGGCGGTGGCGGTATTAACAGATACCTGACTAGGTTATCAAGAGGCTCGACGTT 360
    |||
DB 885 ATAACCGGCGGTGGCGGTATTAACAGATACCTGACTAGGTTATCAAGAGGCTCGACGTT 944
QY 361 GTGAGCTCAACCGGATTTTCAACGTCGAGACATGATGCGCGCGCAAAAGAAAGAG 420
    |||
DB 945 GTGAGCTCAACCGGATTTTCAACGTCGAGACATGATGCGCGCGCAAAAGAAAGAG 1004
QY 421 AAGGGGGCCCTTCAGAGCCCTCGTCTGCTGTCTGCTGATTAAGGCGCGACGCG 480
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DB 1005 AAGGGGGCCCTTCAGAGCCCTCGTCTGCTGTCTGCTGATTAAGGCGCGACGCG 1064
QY 481 GAGGACAACTACTGTCTCAATCTATAGAAAAGACTACAGGAAATGTGGCGACGTACAAC 540
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DB 1065 GAGGACAACTACTGTCTCAATCTATAGAAAAGACTACAGGAAATGTGGCGACGTACAAC 1124
QY 541 CTATCTGAATGGCGCGCTCAATCTGACAGATGTGGGAGTGGACATATGCTCTAGCAC 600
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DB 1125 CTATCTGAATGGCGCGCTCAATCTGACAGATGTGGGAGTGGACATATGCTCTAGCAC 1184
QY 601 CTTTATCTCGGAATGCGCGGAGTACTATATCTCCCACTGCTCGCTCTGCG 660
    |||
DB 1185 CTTTATCTCGGAATGCGCGGAGTACTATATCTCCCACTGCTCGCTCTGCG 1244
QY 661 CAATCTCTGACCTGAAAAATCGGAGATTTGCGCAAAAGCTCTCTAGAACTAGAA 720
    |||
DB 1245 CAATCTCTGACCTGAAAAATCGGAGATTTGCGCAAAAGCTCTCTAGAACTAGAA 1304
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    |||
DB 1305 GTTAAAGATCGCTGTTTAAAGATCGGTCGCACTTACTTTTACCGCGCAAAAGCTG 1364
QY 781 ACAACAGAACTATACAGTGTGATTCAGAGCGAACACCTTTATCCGATCGCACAGACC 840
    |||
DB 1365 ACAACAGAACTATACAGTGTGATTCAGAGCGAACACCTTTATCCGATCGCACAGACC 1424
QY 841 AATACAGCAGCAGGAGAGATATGCGGATACGAAGATATCTGACGCGCTGGAAT 900
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DB 1425 AATACAGCAGCAGGAGAGATATGCGGATACGAAGATATCTGACGCGCTGGAAT 1484
QY 901 AATTTGCTGAGGAAAAAATCTTAGCGCGCAGACCTCTGCGCATAGGCTCCCGAA 960
    |||
DB 1485 AATTTGCTGAGGAAAAAATCTTAGCGCGCAGACCTCTGCGCATAGGCTCCCGAA 1544
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DB 1545 GAAATTCCTGCTTACCAAGAAAGCGAAGGCGCACCCCGGAGCGCAAGAAAGAGCGAA 1604
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DB 1605 AAGAAGCCCCCTCCAGAAAGACTCGGAGAGACATGACGACAGAGCTTTGAGAAAT 1664
QY 1081 CTTGCGCCCTCCCGCAAGACGAGAAAGTCCCGAGAGACACGAGACAGTATCCAAAC 1140
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DB 1665 CTTGCGCCCTCCCGCAAGACGAGAAAGTCCCGAGAGACACGAGACAGTATCCAAAC 1724
QY 1141 TCGATCTGACTATTAAATGACATGCCCGCGTATCCCGGTGAGAGAGACTATAA 1200
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DB 1725 TCGATCTGACTATTAAATGACATGCCCGCGTATCCCGGTGAGAGAGACTATAA 1784
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DB 1785 AGTTTAATGCGCTCCCATGATGCGGCGCTTGTGTAGCTTGGCGGCTGCTC 1844
QY 1261 GTGGGCGCTACTGTTTGGAGCATCTGAAATGCGCGCTGAGCTAA 1305
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DB 1845 GTGGGCGCTACTGTTTGGAGCATCTGAAATGCGCGCTGAGCTAA 1889
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## RESULT 2

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US-09-790-399-7
; Sequence 7, Application US/09790399
; Patent No. US20020038000A1
; GENERAL INFORMATION:
; APPLICANT: Gold, Larry
; APPLICANT: Tuerk, Craig
; APPLICANT: Pridnow, David
; APPLICANT: Smith, Jonathan D.
; TITLE OF INVENTION: Systematic Polypeptide Evolution by Reverse Translation
; FILE REFERENCE: NEX02/CI-COM2
; CURRENT APPLICATION NUMBER: US/09/790,399
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 09/197,649
; PRIOR FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: 07/829,461
; PRIOR FILING DATE: 1992-01-31
; PRIOR APPLICATION NUMBER: 07/739,055
; PRIOR FILING DATE: 1991-08-01
; PRIOR APPLICATION NUMBER: 07/561,968
; PRIOR FILING DATE: 1990-08-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 7
; LENGTH: 390
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence
; OTHER INFORMATION: having a 120 repeat of ACG flanked by fixed
; OTHER INFORMATION: fragments having NcoI restriction sites.
US-09-790-399-7
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Query Match 3.2%; Score 41.6; DB 10; Length 390;  
Best Local Similarity 51.6%; Pred. No. 0.0014;  
Matches 95; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

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QY 1063 GAGGCTTCTGAGAAATTCCTGCGCGCTCCCGCAAGAGAGAGAGAGAGAGAGAGAG 1122
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DB 261 GAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 320
QY 1123 GAGCAGATGATCCAAATCGGATCTGACTATTACAATGATGCGCGCGCTGATCCG 1182
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QY 1183 GTGG 1186
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DB 381 ATGG 384
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RESULT 3
US-09-974-300-5249
Sequence 5249, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
TITLE OF INVENTION: Methods for Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085-500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5249
LENGTH: 863
TYPE: DNA
ORGANISM: Bacillus clausii
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(863)
OTHER INFORMATION: n = A,T,C or G
US-09-974-300-5249

Query Match          2.7%, Score 34.6; DB 10; Length 863;
Best Local Similarity 45.7%; Pmed. No. 0.48;
Matches 121; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

QY  992  CAGACCCCTGCGCCACATGATGCGCCGCGCAAGAAATCCCGCTGTAAACAAGAAAGCGGAG 991
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DB   62  CGGACGCCGATGCCGATGCGGATGCGGACGCCGATGCCGATGCCGATGCTGACGCGGATG 121
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  993  GCGGCACCCCGGACGACAGAAAGCAGCAAAAGCAAAAGAGCCCTTCAGAGACTGCGAGAGC 1051
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB   122  CGGACGCCGATGCCGATGCCGACGCGTGAACGCCGATGCCGAGACGCTGATGGGATGGATG 181
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  1052  ACATCAGACGACAGAGCTTCTGGAGAAATCTCTGCCGCCCTCCCCGAGACGACGAACTCC 1111
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB   182  CGGACGACAGACGCGGACGACCTGATGCTGATGCTGACGCGGACGCCGATGCCGCGGATG 241
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  1112  CCGAGGACACGAGACGATGATCCAAACTCGATCTGATATTAACAATGATGATGCCCG 1171
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DB   242  CGGACGCCGATGCCGATGCCGATGCCGACGCGGACGCTGATGCCGATGCCGATGCTGACG 301
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  1172  CCGTGATCCCGGTGGAGAGAGACTAC 1196
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB   302  CGGATGCCGACGCGGACGCCGATGC 326
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 4
US-09-842-987-1
Sequence 1, Application US/09842987
Patent No. US20020025566A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: ENZYMATIC OXIDATIVE DEAMINATION PROCESS
FILE REFERENCE: HA690
CURRENT APPLICATION NUMBER: US/09/842,987
CURRENT FILING DATE: 2001-04-26
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 1191
TYPE: DNA
ORGANISM: Spingomonas paucimobilis
US-09-842-987-1

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Query Match	2.7%;	Score 34.6;	DB 10;	Length 1191;
Best Local Similarity	49.2%;	Pred. No. 0.58;		
Matches	91;	Conservative	0;	Mismatches 94; Indels 0; Gaps 0;
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DB	685	GGCCATGAAACAAATATGGCGCTGACGCGGACATCATGGCGGTGGCCAAAGGAGCATCGGCGG	744	
OY	994	CGCACCCCGGAGCGCAGAAAGACGCCAAAAGAGGCCCTTCACGAAAGATCTCGAGACGAC	1053	
DB	745	GGCTTCGCGCTGGGGCGGCTCGCTCGCTACCGAGATGCGGCCCAAGGGCATGGTGTTCGGC	804	
OY	1054	ATGCAGGCGAGAGGCTTCTCGAAGAAATCCTCGCGGCTCCCGACGAGACGAGAAGTCCCC	1113	
DB	805	ACCCATGCTTCCACCTATGCGCGCAACCCGCTCGCCATGGCGGTGGGACATCGCGGTCTG	864	
OY	1114	GAGGA	1118	
DB	865	GAGGA	869	
RESULT 5				
US-10-014-717-1				
Sequence 1, Application US/10014717				
Publication No. US20020192778A1				
GENERAL INFORMATION:				
APPLICANT: Schupp, Thomas				
APPLICANT: Ligon, James				
APPLICANT: Molnar, Istvan				
APPLICANT: Zikkle, Ross				
APPLICANT: Cyr, Devon				
APPLICANT: Goelach, Joern				
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES				
FILE REFERENCE: 4-30582A				
CURRENT APPLICATION NUMBER: US/10/014.717				
CURRENT FILING DATE: 2001-11-13				
PRIOR APPLICATION NUMBER: US/09/335,409				
PRIOR FILING DATE: 1999-06-17				
NUMBER OF SEQ ID NOS: 30				
SOFTWARE: Patentin Ver. 2.0				
SEQ ID NO 1				
LENGTH: 68750				
TYPE: DNA				
ORGANISM: Sorangium cellulosum				
US-10-014-717-1				
Query Match	2.6%;	Score 34.4;	DB 9;	Length 68750;
Best Local Similarity	46.3%;	Pred. No. 8;		
Matches	113;	Conservative	0;	Mismatches 131; Indels 0; Gaps 0;
OY	215	TACTGCTTTCCTTCCTTCGCTAGCCAGACGACCCGCCGCTACAGTACGACTCATTTAG	274	
DB	4373	TGCTCTGTGGCGACCGCGAGCGGCGAAGTGTCTCCCGCCGCTCGCGCGGCTCG	4432	
OY	275	GCGGTCGGGCGGTGCAGCGGCTAACCATACGGGGGTTGGGCCGTAATACATACATACCTCA	334	
DB	4433	GGGGGCTAGGGGCGACGCGGCGGCTGTGGGCGGTGGGCTTGAACATGAAGGGCGCA	4492	
OY	335	CTAGAGGTATCAAGAGGCTGCGACGTTGTGAGACTCAACCCGATTTCTTAAGTGAAGACA	394	
DB	4433	CGGACTCATCTCGCGCATCTGCGGCGGTGAGACTCGGGGCTCCTCTTCGAAGAGGCTTATA	4552	
OY	395	TGATATCGGCGGCCAAAGAAAAAGAAAGAGGGGGGCCCTTTGAGAGGCTCCGTCGTGGT	454	
DB	4553	CGATGTACGCGCTGCTCGGCTGTACAGGTTGACCGCTACCCGCGCTCCATCTGTGC	4612	
OY	455	TCTA	458	
DB	4613	TCGA	4616	
RESULT 6				
US-09-864-761-24106				

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; Sequence 24106, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aesomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 24106
; LENGTH: 384
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL121988.10
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.9
; OTHER INFORMATION: NT HIT: AF099731.1, EVALUATE 0.00e+00
; OTHER INFORMATION: EST_HUMAN HIT: BE712515.1, EVALUATE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: O95377, EVALUATE 3.00e-73
US-09-864-761-24106

Query Match      2.6%; Score 34.2; DB 10; Length 384;
Best Local Similarity 49.2%; Pred. No. 0.4;
Matches 90; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
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Qy 1048 GAGCAGATGACAGCGAGCGCTTGTGAGAAAATCTCCGCCCTCCCGAAGACGAGAA 1107
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 139 GACCACAGAGAGGAGGAGATATTTGGGGTAGAATGAGTGAACATAGAGAAAGGCGAT 198
Qy 1108 GTCCCGCAGACACCGACGAGATGATCCAACTCGGATCTGACTATTCATGACATG 1167
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 199 GTCCACCGCTGCGCTTGTGAACACTAGGCTGCAGACATATGTCCACCAAGCCCGCCTT 258
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1168 CCGCCGCTGATCCCGGTGAGAGGAGACTACTAAAGTTCATGCGCTTCATGCCATTA 1227
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 259 CTTCGCGGGGTTCAGTAGAGAGCGCCCACTGTCTCCCATGTGGGCTTCTCGTCTT 318
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1228 TTC 1230
      ||
Db 319 CTC 321

RESULT 7
US-09-864-761-25125
; Sequence 25125, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aesomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 25125
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Homo sapiens
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; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 8395
; LENGTH: 586
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL122010.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.6
US-09-864-761-8395
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Query Match
Best Local Similarity 2.6%; Score 34.2; DB 10; Length 586;
Matches 90; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
QY 1048 GAGCAGATGAGCAGAGGTTGTGAGAAATCTGCGCCCTCCCGAAGAGCAGAA 1107
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DB 341 GAGCAGAGGAGGAGATATATTGGGTAGATGAGTGAACACATAGAGAAAGCGAT 400
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1108 GTCCCGGAGACACGACGATGATCAAACTCGATCCGATCATTAATGACATG 1167
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 401 GTCCAGGCTGCGCTTAACACTGCTGACACATATGTCACCAAGAGCCCGCTT 460
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1168 CCGCGGTGATCCGCTGAGAGAGACTATAAAGTTCTAATGCCCTCTCAATGCCATA 1227
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 461 CTGCGGGGTTCAAGTAGAGCGCCACTGTCTCCCATGGGCTTCTCGGTGCTCTT 520
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1228 TTC 1230
    ||
DB 521 CTC 523
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RESULT 10
US-09-894-998-35/c
; Sequence 35, Application US/09894998
; Patent No. US2002090610A1
; GENERAL INFORMATION:
```

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; APPLICANT: Hosken, Nancy Ann
; APPLICANT: Craig H. Day
; APPLICANT: David C. Dillon
; APPLICANT: McGowan, Patrick
; APPLICANT: Sleath, Paul R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: 210121.538
; CURRENT APPLICATION NUMBER: US/09/894,998
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 2481
; TYPE: DNA
; ORGANISM: HSV-2
US-09-894-998-35
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Query Match
Best Local Similarity 48.2%; Score 34.2; DB 10; Length 2481;
Matches 96; Conservative 0; Mismatches 103; Indels 0; Gaps 0;
QY 927 CGGCGCAGACCTGTCTCAGATAGCGTCCGCAAGAAATCCGCTTAACCAAGAAAGC 986
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1902 CCCACACGCCCCCGCCGACAGAGAGAGCGGAGAGAGAGAGAGAGAGAGAGAGG 1843
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 987 GGAAGGGCGCACCCCGGAGCCAGAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1046
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1842 GGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1783
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1047 GGACGACATGACAGAGAGGCTTCTGAGAAATCTGCGCCCTCCCGAAGAGAGCA 1106
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DB 1782 GGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1723
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1107 AGTCCCGGAGACACCGAG 1125
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DB 1722 GGGCGCCGCGGAGCGCGG 1704
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RESULT 11
US-09-974-300-2209
; Sequence 2209, Application US/0974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2209
; LENGTH: 1038
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-2209
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Query Match
Best Local Similarity 49.4%; Score 34; DB 10; Length 1038;
Matches 88; Conservative 0; Mismatches 90; Indels 0; Gaps 0;
QY 994 GCGACCCGAGCGAGAAAGAGCGCCCTCCGAGAACTCGAGAGAGAGAC 1053
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 783 CGCTTCTGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 842
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1054 ATGACAGAGAGGCTTCTGAGAAATCTGCGCCCTCCCGAAGAGAGAGAAAGTCCC 1113
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

Db 843 TCGGTGGAGGATGATGACTCTGCCGCAAAATCGGTGATGCAAGAAAAAGATGCC 902  
QY 1114 GAGACACCGAGCAGATGATCCAAATCGATCTTCACTTTTCAATGACATGCCG 1171  
Db 903 GCCAACCTTGTACATGCCAACAAACCGAGATCTTGCCTATTACATTATACATCCG 960

## RESULT 12

US-09-938-842A-125  
; Sequence 125, Application US/09938842A  
; Patent No. US20020160378A1  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; FILE REFERENCE: S1300-3  
; CURRENT APPLICATION NUMBER: US/09/938,842A  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/300,111  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 125  
; LENGTH: 438  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-125

Query Match 2.6%; Score 33.6; DB 9; Length 438;  
Best Local Similarity 52.1%; Pred. No. 0.69;

Matches 75; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1002 GAGCGCAAGAAAGCAAGAAAGCCCTCCAGAACTCGAGAGCATGACAGC 1061  
Db 265 GAGGAGCGTACCAAGAGGAGGAGCATACCAAGAGCGGCGGCGCAAGAGGAG 324  
QY 1062 AGAGCGTTCTGGAGAAATCTCGCCGCCCGGAGAGAGCAATCCCGGAGAC 1121  
Db 325 GGGGGAAGTGGGGAATTTCTGCCGCGCAGCGCTGCTACTACAGAGTTTCAACGGCTGC 384  
QY 1122 CGAGCAGATGATCAAACTCGA 1145  
Db 385 TCAAGATGCTGCTGCTATGCCGA 408

## RESULT 13

US-09-770-149-358/C  
; Sequence 358, Application US/09770149  
; Patent No. US2002005963A1  
; GENERAL INFORMATION:  
; APPLICANT: Goriach, Jörn  
; APPLICANT: An, Yong-Qiang  
; APPLICANT: Hamilton, Carol M.  
; APPLICANT: Price, Jennifer L.  
; APPLICANT: Raines, Tracy M.  
; APPLICANT: Yu, Yang  
; APPLICANT: Rameaka, Joshua G.  
; APPLICANT: Page, Amy  
; APPLICANT: Mathew, Abraham V.  
; APPLICANT: Ledford, Brooke L.  
; APPLICANT: Moessner, Jeffrey P.  
; APPLICANT: Haas, William David  
; APPLICANT: Garcia, Carlos A.  
; APPLICANT: Krickler, Maja  
; APPLICANT: Slader, Ted  
; APPLICANT: Davis, Keith R.  
; APPLICANT: Allen, Keith

; APPLICANT: Hoffman, Neil  
; APPLICANT: Hurban, Patrick  
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis  
; FILE REFERENCE: 2024 (PARA-013PRV)  
; CURRENT APPLICATION NUMBER: US/09/770,149  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 60/178,506  
; PRIOR FILING DATE: 2000-01-27  
; NUMBER OF SEQ ID NOS: 999  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 358  
; LENGTH: 678  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-770-149-358

Query Match 2.6%; Score 33.6; DB 10; Length 678;  
Best Local Similarity 52.1%; Pred. No. 0.89;  
Matches 75; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1002 GAGCGCAAGAAAGCAAGAAAGCCCTCCAGAACTCGAGAGCATGACAGC 1061  
Db 403 GAGGAGCGTACCAAGAGGAGGAGCATACCAAGAGCGGCGGCGCAAGAGGAG 344  
QY 1062 AGAGCGTTCTGGAGAAATCTCGCCGCCCGGAGAGAGCATGACAGAGC 1121  
Db 343 GGGGGAAGTGGGGAATTTCTGCCGCGCAGCGCTGCTACTACAGAGTTTCAACGGCTGC 284  
QY 1122 CGAGCAGATGATCAAACTCGA 1145  
Db 283 TCAAGATGCTGCTGCTATGCCGA 260

## RESULT 14

US-09-938-842A-1892/C  
; Sequence 1892, Application US/09938842A  
; Patent No. US20020160378A1  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; FILE REFERENCE: S1300-3  
; CURRENT APPLICATION NUMBER: US/09/938,842A  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/300,111  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 1892  
; LENGTH: 1503  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-1892

Query Match 2.6%; Score 33.6; DB 9; Length 1503;  
Best Local Similarity 57.7%; Pred. No. 1.4;  
Matches 60; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 890 AGCGCTGGAATTAATTTCTGAGAAAAAGATCTACGCGCAGACCTGTCACATA 949  
Db 388 ATGCTTCAAGTAAGCCCAAGCATTTGCAATTTTCTGCTCCAAACGTTTGACATA 329  
QY 950 GCGTCCGCAAGAAATTCGCGTGTAAACAAGAAAGCGGAAGG 993  
Db 328 GCGTTCTAAGCAGCTCCATTCGAAGCATGATGCCGATGAG 285

## RESULT 15

US-09-819-104A-6

; Sequence 6, Application US/09819104A

; Publication No. US20030027137A1

; GENERAL INFORMATION:

; APPLICANT: Chen, J. Don

; TITLE OF INVENTION: NOVEL NUCLEAR RECEPTOR COREPRESSOR MOLECULES

; TITLE OF INVENTION: AND USES THEREFOR

; FILE REFERENCE: UMG-030

; CURRENT APPLICATION NUMBER: US/09/819,104A

; PRIOR APPLICATION NUMBER: 2001-03-27

; PRIOR FILING DATE: 2000-03-29

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 6

; LENGTH: 7386

; TYPE: DNA

; ORGANISM: Mus musculus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(7386)

; US-09-819-104A-6

Query Match 2.5%; Score 33.2; DB 9; Length 7386;

Best Local Similarity 52.1%; Pred. No. 5.2;

Matches 74; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

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QY 997 ACCCCGACGCAAAAGCAGCAAAAGAGCCCTCCAGAGACTCGAGAGACGACATG 1056
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Db 2044 ACCCCAGCTCGGCGAGGAGACAGCCTTCCACCTCCGCTGAGGAGAGAGATG 2103
      ||| | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1057 CAGGCAAGAGGCTTCTGAGAGAAATCTGCCGCCCTCCCGAGAGAGCAAGTCCCGAG 1116
      ||| | | | | | | | | | | | | | | | | | | | | | | | |
Db 2104 GAGCATCAGGCGCAAGTGCATGAGAGAGAGCTGGCGGAGAGGCGAGAGGCTCACAG 2163
      ||| | | | | | | | | | | | | | | | | | | | | | | | |
QY 1117 GACACCGAGCAGATGATCCAA 1138
      | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2164 GCCTCTGGAAATGAGGTTCCCA 2185
      | | | | | | | | | | | | | | | | | | | | | | | | |
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Search completed: February 25, 2003, 15:49:15  
Job time : 108 secs

GenCore version 5.1.3  
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## OM nucleic - nucleic search, using sw model

Run on: February 25, 2003, 12:53:59 ; Search time 3584 Seconds

(without alignments)  
10596.864 Million cell updates/sec

Title: US-09-994-064-10

Perfect score: 1305  
Sequence: 1 ATGCACCGCTCCTCATCTCAG.....TAAATGCCGCGCTACTATA 1305

## Scoring table:

IDENTITY\_NDC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 1008  
Listing first 45 summaries

## Database :

GenEmbl: \*  
1: gb\_ba: \*  
2: gb\_hlg: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
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8: gb\_pl: \*  
9: gb\_pr: \*  
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11: gb\_sts: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
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16: em\_fun: \*  
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28: em\_un: \*  
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33: em\_hlg\_mus: \*  
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35: em\_hlg\_rtd: \*  
36: em\_hlg\_mam: \*  
37: em\_hlg\_vrt: \*  
38: em\_sy: \*  
39: em\_higo\_hum: \*  
40: em\_higo\_mus: \*  
41: em\_higo\_other: \*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1305	100.0	1305	6	AR093367	AR093367 Sequence
2	1305	100.0	1305	6	AR135449	AR135449 Sequence
3	1305	100.0	18912	14	ILU28832	U28832 Infectious
4	1268.2	97.2	1627	14	HSWGDGLYCO	L31965 Gallid herp
5	361	27.7	3502	6	A22122	A22122 ILTV gp60 g
6	52.2	4.0	161046	14	AF081810	AF081810 Lymantria
7	45.8	3.5	2676	1	MXARPOD	M32347 M.xanthus s
8	45.8	3.5	7980	1	MXU20669	U20669 Myxococcus
9	44.4	3.4	7218	6	166494	166494 Sequence 14
10	44.4	3.4	185863	2	AC121079	AC121079 Mus muscu
11	43.6	3.3	99360	8	NCB11N2	AL513444 Neurospor
12	43.4	3.3	125020	9	AF429315	AF429315 Homo sapi
13	43	3.3	3022	8	SCYOR053W	Z70678 S.cerevisia
14	42.8	3.3	54719	2	AC104329	AC104329 Mus muscu
15	41.2	3.2	202761	2	AC104329	AC104329 Mus muscu
16	41.8	3.2	181003	2	AC127549	AC127549 Mus muscu
17	41.8	3.2	181931	2	AC115847	AC115847 Mus muscu
18	41.6	3.2	390	6	AR135147	AR135147 Sequence
19	41.4	3.2	149333	2	AP004592	AP004592 Oryza sat
20	41.2	3.2	191584	2	AC120477	AC120477 Rattus no
21	41	3.1	67392	2	AC110550	AC110550 Mus muscu
22	40.8	3.1	187466	2	AC102480	AC102480 Mus muscu
23	40.6	3.1	158955	2	AC115344	AC115344 Rattus no
24	40.4	3.1	158531	2	AC119294	AC119294 Rattus no
25	40.4	3.1	195549	2	AC012019	AC012019 Homo sapi
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27	40	3.1	23407	1	RSO245811	AJ245811 Ralstonia
28	40	3.1	30350	8	YSC9315	U10398 Saccharomyc
29	40	3.1	194334	2	AC101527	AC101527 Mus muscu
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## ALIGNMENTS

RESULT 1  
AR093367 1305 bp DNA linear PAT 08-SEP-2000  
LOCUS  
DEFINITION Sequence 19 from patent US 6001369.  
ACCESSION AR093367  
VERSION AR093367.1 GI:10020117  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1305)  
AUTHORS Cochran, M.D. and Junker, D.E.  
TITLE Recombinant fowlpox viruses and uses thereof  
JOURNAL Patent: US 6001369-A 19 14-DEC-1999;  
FEATURES Location/Qualifiers

source 1.1305 /organism="unknown"  
BASE COUNT 331 a 349 c 344 g 281 t  
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DEFINITION Sequence 19 from patent US 6136318.  
ACCESSION ARI35449  
VERSION ARI35449.1 GI:14476121  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1305)  
AUTHORS Cochran,M.D. and Junker,D.E.  
TITLE Recombinant fowlpox viruses and uses thereof  
JOURNAL Patent: US 6136318-A 19 24-Oct-2000;  
FEATURES  
source location/qualifiers  
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BASE COUNT 331 a 349 c 344 g 281 t  
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Query Match 100.0%; Score 1305; DB 6; Length 1305;  
Best Local Similarity 100.0%; Pred. No. 0;  
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RESULT 3
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DEFINITION
Infectious laryngotracheitis virus US10, US2, protein kinase, UL47,
glycoprotein G, ORF5, glycoprotein D, glycoprotein I, glycoprotein
E, ORF9 genes, complete cds.
ACCESSION
U28832
VERSION
U28832.1 GI:1486484

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KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
repeat_region
CDS
CDS
CDS
CDS

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Infectious laryngotracheitis virus.  
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 Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
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 1 (bases 1 to 18912)  
 Wild,M.A., Cook,S. and Cochran,M.  
 A genomic map of infectious laryngotracheitis virus and the  
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Accession	Version	Keywords	Source	Organism	Reference Authors	Title	Journal	Medline	PubMed	Features
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L31965.1	GI:493595	glycoprotein D, GaIIid herpesvirus 1, GaIIid herpesvirus 1, viruses: dsDNA viruses, no RNA stage: Herpesviridae: Alphaherpesvirinae: Infectious laryngotracheitis-like viruses.								
1 (bases 1 to 1627)										
Johnson, M. A., Tyack, S. G., Prideaux, C. T., Kongsuwan, K. and Sheppard, M.										
Sequence characteristics of a gene in infectious laryngotracheitis virus homologous to glycoprotein D of herpes simplex virus										
DNA Seq. 5 (3), 191-194 (1995)										
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LOCUS ILTV gp60 gene.
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KEYWORDS
SOURCE Gallid herpesvirus 1.
ORGANISM Gallid herpesvirus 1
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Query Match 27.7%; Score 361; DB 6; Length 3502;
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RESULT 6
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LOCUS Lymantria dispar nucleopolyhedrovirus, complete genome.
DEFINITION AF081810
ACCESSION AF081810.1 GI:3822234
VERSION
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REFERENCE 1 (bases 4593 to 7280)  
AUTHORS Inouye, S.  
TITLE Cloning and DNA sequence of the gene coding for the major sigma  
factor from Myxococcus xanthus  
JOURNAL J. Bacteriol. 172 (1), 80-85 (1990)  
MEDLINE 90094274  
PUBMED 2104614  
REFERENCE 2 (bases 1 to 7980)  
AUTHORS Davis, J.M., Mayor, J. and Plamann, L.  
TITLE A missense mutation in rpoD results in an A-signalling defect in  
Myxococcus xanthus  
JOURNAL Mol. Microbiol. 18 (5), 943-952 (1995)  
MEDLINE 96422481  
PUBMED 8825098  
REFERENCE 3 (bases 1 to 7980)  
AUTHORS Plamann, L.S.  
TITLE Direct Submission  
JOURNAL Submitted (06-FEB-1995) Lynda S Plamann, Department of Biology,  
Texas A & M University, College Station, TX 77843-3258, USA  
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Mus musculus chromosome, clone RP24-178P12  
unpublished  
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Birren,B., Linton,L., Nusbaum,C., Lande,E., All,A., Allen,N.,  
Anderson,S., Barina,N., Bastien,V., Bloom,T., Boguslavsky,L.,  
Bookhalter,B., Brown,A., Camarata,J., Campotiano,A., Chang,J.,  
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Kamat,A., Karatas,A., Kells,C., Larocque,K., Lamazares,R.,  
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Raymond,C., Retta,R., Ribback,M., Riley,R., Rise,C., Rogov,P.,  
Roman,J., Rossetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,  
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,  
Strassus,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,  
Topham,K., Travers,M., Travis,N., Triggillo,J., Vassiliev,H.,  
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,  
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.  
Direct Submission  
Submitted (15-MAY-2002) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
3 (bases 1 to 185863)  
Birren,B., Nusbaum,C., Lande,E., All,A., Allen,N., Anderson,S.,  
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Submitted (21-AUG-2002) Whitehead Institute/MIT Center for Genome  
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On Aug 21, 2002 this sequence version replaced gi:20806332.  
All repeats were identified using RepeatMasker:  
Smith, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html  
Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence.submissions@genome.wi.mit.edu  
Project Information



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Center clone name: 178_P12
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Chemistry: Dye-terminator Big Dye; 100% of reads
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Quality coverage: 10.8 in Q20 bases; sum-of-contigs
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* consists of 16 contigs. Gaps between the contigs
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* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
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DR P-PSDB: AAR58856.  
 XX New recombinant fowl pox virus for use in vaccines - contains  
 PT genes expressing antigens of Newcastle disease virus and opt.  
 PT infectious bronchitis virus  
 XX  
 PS Disclosure: Page 74-75; 85pp; English.  
 XX  
 CC AA068944 contains the coding region of the ILT gd gene and was  
 CC derived from an approx. 2060 bp EcoRI to BclI restriction sub-  
 CC fragment of the ILT KpnI genomic restriction fragment #8 (10.6kb).  
 CC It is part of a cassette in plasmid 586-36.6 constructed for  
 CC the purpose of inserting ILT gb and gd genes into the fowlpox  
 CC virus (FPV).  
 XX  
 SQ Sequence 1305 BP; 331 A; 349 C; 344 G; 281 T; 0 other;

Query Match 100.0%; Score 1305; DB 15; Length 1305;  
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 Db 1141 TCGGATCTGACTATTAATGACATGACCGCGCTGATCCCGGTGAGAGACTACTAA 1200  
 QY 1201 AGTTTAATGCCGTCTCCATGCCCATAATTCGCGGCTGCTAGCGCGGTGCGGCTC 1260  
 Db 1201 AGTTTAATGCCGTCTCCATGCCCATAATTCGCGGCTGCTAGCGCGGTGCGGCTC 1260  
 QY 1261 GTGGGGCTACTGTTTGGAGCATCTGTAATATGCGCGCTGAGCTAA 1305  
 Db 1261 GTGGGGCTACTGTTTGGAGCATCTGTAATATGCGCGCTGAGCTAA 1305

RESULT 2  
 AAT33505  
 ID AAT33505 standard; DNA; 1305 BP.

XX AAT33505;  
 XX  
 DT 19-NOV-1996 (first entry)  
 XX

DE Infectious laryngotracheitis virus gd gene.  
 XX  
 XX Infectious laryngotracheitis virus; ILTV; herpesvirus;  
 KW attenuation; vector; vaccine; chicken; poultry; immunisation;  
 KW glycoprotein gd; ds.  
 XX

OS Infectious laryngotracheitis virus.  
 XX

PN W09508622-AL.  
 XX

PD 30-MAR-1995.  
 XX

PF 16-SEP-1994; 94WO-US10628.  
 XX

PR 24-SEP-1993; 93US-0126597.  
 XX

XX (SYTR ) SYNTRO CORP.  
 XX

PA Cochran MD, Wild MA;  
 XX

XX WPI; 1995-139591/18.  
 DR

XX P-PSDB; AAM00638.  
 XX

PT Recombinant attenuated infectious laryngotracheitis virus - for use  
 PT in vaccines to protect poultry from infection from the virus, also  
 PT methods of distinguishing between vaccinated and naturally infected  
 PT birds  
 XX



PS Example 1; Page 106-107; 177pp; English.

CC The gd gene (AAT33505) spans bases 8462-9766 of the unique short  
CC region (see also AAT33504) of infectious laryngotracheitis virus  
CC (ILTV) genomic DNA. It codes for a glycoprotein (AAM00638) of  
CC approx. 48,477 mol.wt. that is homologous to pseudorabies  
CC virus gD and to gd from herpes simplex virus-1. Marek's  
CC disease virus, IPV and bovine herpesvirus-1.1. Monoclonal  
CC antibodies raised to ILTV react specifically with gd from  
CC ILTV and also with ILTV gd expressed in herpesvirus of  
CC turkeys (HVT) virus vector. ILTV gd expressed in the HVT  
CC vector is useful as a subunit vaccine.

XX Sequence 1305 BP; 331 A; 349 C; 344 G; 281 T; 0 other;

Query Match: 100.0%; Score 1305; DB 16; Length 1305;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 ATGCACCGTCTCATCTCAGACGGCACCTGCCCTTACTACCGGAAGAGAGTGTAAAC 60
DB 1 ATGCACCGTCTCATCTCAGACGGCACCTGCCCTTACTACCGGAAGAGAGTGTAAAC 60
QY 61 AACACATGATGATGCGGTGAAAACGGTCTGCTCAGAGCCAGCTGTAATCAGCTTTTC 120
DB 61 AACACATGATGATGCGGTGAAAACGGTCTGCTCAGAGCCAGCTGTAATCAGCTTTTC 120
QY 121 TGACATGTTGTCAGATTATGCGGAGACATATCTGCTTTGACGCAAGCTATGAGCCG 180
DB 121 TGACATGTTGTCAGATTATGCGGAGACATATCTGCTTTGACGCAAGCTATGAGCCG 180
QY 181 CATTATTTTGAAGAAATGTTTTTGGACATATGTAATGCTTTCTTCTTCTGCTAGCAG 240
DB 181 CATTATTTTGAAGAAATGTTTTTGGACATATGTAATGCTTTCTTCTTCTGCTAGCAG 240
QY 241 AGCAGCGCCGCTCAGATGACATATTTAGCGCGCTGCGCGCTCAGCGCTAAC 300
DB 241 AGCAGCGCCGCTCAGATGACATATTTAGCGCGCTGCGCGCTCAGCGCTAAC 300
QY 301 ATACCGGCGTGGCCGCTATTAACAGATCCTCAGTAGGGTATCAAGAGCTCGACGTT 360
DB 301 ATACCGGCGTGGCCGCTATTAACAGATCCTCAGTAGGGTATCAAGAGCTCGACGTT 360
QY 361 GTGAGCTCAACCCGATTTCTAAGCGTAGAGATATATGCGCGCAAGAAAAGAG 420
DB 361 GTGAGCTCAACCCGATTTCTAAGCGTAGAGATATATGCGCGCAAGAAAAGAG 420
QY 421 AAGGGGGGCCCTTTCAGAGGCTCCGTCGTGTTTACGTGATTAAGGCGCAGACGC 480
DB 421 AAGGGGGGCCCTTTCAGAGGCTCCGTCGTGTTTACGTGATTAAGGCGCAGACGC 480
QY 481 GAGGACAGTACTGTCCATCTATAGAAAAGATACAGGGAATGTGGCAGCTACAACTG 540
DB 481 GAGGACAGTACTGTCCATCTATAGAAAAGATACAGGGAATGTGGCAGCTACAACTG 540
QY 541 CTATCTGAATGCGCGCTTCAATCTGACAGATGTGGCAATGTGACATATCTTCTAGCACC 600
DB 541 CTATCTGAATGCGCGCTTCAATCTGACAGATGTGGCAATGTGACATATCTTCTAGCACC 600
QY 601 CTGTGATCGGAATGCGCGGAGTACATATTTCCGCCACTGCTGCGCTCTGCGG 660
DB 601 CTGTGATCGGAATGCGCGGAGTACATATTTCTCCGCCACTGCTGCGCTCTGCGG 660
QY 661 CAATACTTCTGACCTGAAAATCGGAGATTTGCGCAAAACAGCTCTGTAATCTAGAA 720
DB 661 CAATACTTCTGACCTGAAAATCGGAGATTTGCGCAAAACAGCTCTGTAATCTAGAA 720
QY 721 GTTAAGGATCGCTGTTTAAAGATCGGGTGCAGCTTAATCTTTTACCCTGGAATGCTGG 780
DB 721 GTTAAGGATCGCTGTTTAAAGATCGGGTGCAGCTTAATCTTTTACCCTGGAATGCTGG 780
QY 781 ACAAGACAGATATCAGACTGATTTCAAGGGAACACTTATCTCGATCGCAGACACC 840
DB 781 ACAAGACAGATATCAGACTGATTTCAAGGGAACACTTATCTCGATCGCAGACACC 840
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DB 781 ACAAGACAGATATCAGACTGATTTCAAGGGAACACTTATCTCGATCGCAGACACC 840
QY 841 AATACAGACACGCGGAGCAGATATATCGGGATACGAGAATATTTGACGCGTGAAT 900
DB 841 AATACAGACACGCGGAGCAGATATATCGGGATACGAGAATATTTGACGCGTGAAT 900
QY 901 AATTGTGTGAGAAAAAAGATTCCTAGCGCGCCAGACCTCTGTCCAGATACCGTCCGCA 960
DB 901 AATTGTGTGAGAAAAAAGATTCCTAGCGCGCCAGACCTCTGTCCAGATACCGTCCGCA 960
QY 961 GAAATTCCTCTGTAACCAAGAAAGCGGAGCGCACCCCGGACGAGAAAGCAGGAA 1020
DB 961 GAAATTCCTCTGTAACCAAGAAAGCGGAGCGCACCCCGGACGAGAAAGCAGGAA 1020
QY 1021 AAGAAGCCCTCCCAAGAAAGCTCGGAGACGACATGCAAGCAGAGCTTTGAGAAAT 1080
DB 1021 AAGAAGCCCTCCCAAGAAAGCTCGGAGACGACATGCAAGCAGAGCTTTGAGAAAT 1080
QY 1081 CCTGCGCGCTCCCGGAGAGCAAGAGTCCCGGAGACACGACGATGATCCAAAC 1140
DB 1081 CCTGCGCGCTCCCGGAGAGCAAGAGTCCCGGAGACACGACGATGATCCAAAC 1140
QY 1141 TCGGATCTGACTATTTACATGACATGCCCGCTGATCCCGGTGAGAGACTACTAAA 1200
DB 1141 TCGGATCTGACTATTTACATGACATGCCCGCTGATCCCGGTGAGAGACTACTAAA 1200
QY 1201 AGTTCTAATCCGCTCTCCATGCCCCATATTCGCGCGCTTCTGACCTGCGCGCTC 1260
DB 1201 AGTTCTAATCCGCTCTCCATGCCCCATATTCGCGCGCTTCTGACCTGCGCGCTC 1260
QY 1261 GTGGGGCTACTGTTTGGAGCATGCTAAATGGCGCGGTAGCTAA 1305
DB 1261 GTGGGGCTACTGTTTGGAGCATGCTAAATGGCGCGGTAGCTAA 1305

RESULT 3
AAX81152
ID AAX81152 standard; DNA: 1305 BP.
XX AC AAX81152;
XX DT 07-SEP-1999 (first entry)
XX DE Seq ID No: 19 of US925358.
XX KW Fowlpox virus; FPV; recombinant; vaccine; immunisation; chicken; NDV; Newcastle disease virus; NDV; Fowlpox; Infectious laryngotracheitis; ds.
XX OS Fowlpox virus.
XX PN US925358-A.
XX PD 20-JUL-1999.
XX PE 07-JUN-1995; 95US-0484575.
XX PR 07-JUN-1995; 95US-0484575.
XX PR 26-FEB-1993; 93US-0024156.
XX PR 28-FEB-1994; 94WO-US02252.
XX PA (SYTR ) SYNTRO CORP.
XX PI Cochran MD, Junker DE;
XX DR WPI: 1999-418249/35.
XX DR P-PSDB: AAY21984.
XX PT Fowlpox viruses, useful as vaccines for immunization of
XX PS chickens/turkeys against Fowlpox and Newcastle disease. virus
XX OS disclosure; Columns 77-82; 108bp; English.
XX CC The invention relates to a recombinant fowlpox virus (FPV) comprising
```

CC a foreign DNA inserted into a region of the fowlpox virus genome  
 CC corresponding to a 2.8 kb EcoRI fragment, capable of being expressed in a  
 CC host cell. The virus is used as a vaccine for immunising chickens against  
 CC Newcastle disease virus (NDV), Fowlpox, and infectious laryngotracheitis.  
 XX

Sequence 1305 BP; 331 A; 349 C; 344 G; 281 T; 0 other;

Query Match 100.0%; Score 1305; DB 20; Length 1305;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGACCGCTCTATCTCAGACGGGCTGCGTTACTACGCGAAGAGAGAGGCTTTAAC 60
DB 1 ATGACCGCTCTATCTCAGACGGGCTGCGTTACTACGCGAAGAGAGAGGCTTTAAC 60
QY 61 AACACATGATGCGGTGGAAAAAGGTGCTGCTCAGGCGCCAGCTGATTCATCTTTTC 120
DB 61 AACACATGATGCGGTGGAAAAAGGTGCTGCTCAGGCGCCAGCTGATTCATCTTTTC 120
QY 121 TGGACTTGTGTAGAGATTATGCGGAGCATATCTGCTTTAGCAACGCTATGACCGC 180
DB 121 TGGACTTGTGTAGAGATTATGCGGAGCATATCTGCTTTAGCAACGCTATGACCGC 180
QY 181 CATTTATTTTGAAGAAATGCTTTTGGACTATGTAAGCTTCTTCTGCTAGCCAG 240
DB 181 CATTTATTTTGAAGAAATGCTTTTGGACTATGTAAGCTTCTTCTGCTAGCCAG 240
QY 241 AGCACCGCGCCGCTCAGTACGATCAATTTTAGCGCGCGCGCTGCGGCTAACCC 300
DB 241 AGCACCGCGCGCTCAGTACGATCAATTTTAGCGCGCGCGCTGCGGCTAACCC 300
QY 301 ATACCGCGGTGGCGCCGCTATTAACAGATCCTCAGTATCAAGAGGCTGCGACGTT 360
DB 301 ATACCGCGGTGGCGCCGCTATTAACAGATCCTCAGTATCAAGAGGCTGCGACGTT 360
QY 361 GTGAGCTCAACCCGATTTCTAAGTGAAGAGATATGCGGCGCCAAAGAAAAAGAG 420
DB 361 GTGAGCTCAACCCGATTTCTAAGTGAAGAGATATGCGGCGCCAAAGAAAAAGAG 420
QY 421 AAGGGGGGCGCTTTGAGGCGCTCCGCTGCTGCTGCTTACAGTAAAGGCGCGACGCG 480
DB 421 AAGGGGGGCGCTTTGAGGCGCTCCGCTGCTGCTGCTTACAGTAAAGGCGCGACGCG 480
QY 481 GAGGACAACTACTGCTCAATCTATAGAAAAAGATACAGGAAATGTCGCGACGTACA 540
DB 481 GAGGACAACTACTGCTCAATCTATAGAAAAAGATACAGGAAATGTCGCGACGTACA 540
QY 541 CTATCTGAATGCGCGCTCAATCTGACAGATGTGGGCGAGTGTCTCTAGCAGCC 600
DB 541 CTATCTGAATGCGCGCTCAATCTGACAGATGTGGGCGAGTGTCTCTAGCAGCC 600
QY 601 CTTGTATGCGGAAATGCGCGGAGCTGACTATATCTCCCGACATGCTGCGCTCTG 660
DB 601 CTTGTATGCGGAAATGCGCGGAGCTGACTATATCTCCCGACATGCTGCGCTCTG 660
QY 661 CATATCTGCTGACCTGAAAAATCGGAGATTTGGGCAAAAGCTCTGTAACTAGAA 720
DB 661 CATATCTGCTGACCTGAAAAATCGGAGATTTGGGCAAAAGCTCTGTAACTAGAA 720
QY 721 GTTAAAGATCGCTGTTTAAAGATCGGTCGACGTTAACTTTTACCGTCAAGATG 780
DB 721 GTTAAAGATCGCTGTTTAAAGATCGGTCGACGTTAACTTTTACCGTCAAGATG 780
QY 781 ACAACAGAACTATCAAGCTGATTTCAAGCGCAACCTTTATCCGATCGCAGACAC 840
DB 781 ACAACAGAACTATCAAGCTGATTTCAAGCGCAACCTTTATCCGATCGCAGACAC 840
QY 841 AATACACACACGCGGAGAGATATGCGGATACGAAGATATCTGACAGCGCTGGA 900
DB 841 AATACACACACGCGGAGAGATATGCGGATACGAAGATATCTGACAGCGCTGGA 900
QY 901 AATTGCTAGAGAAAAAAGATCTAGCGCGACGCTCTCCGATAGAGGTCCCGCAA 960
DB 901 AATTGCTAGAGAAAAAAGATCTAGCGCGACGCTCTCCGATAGAGGTCCCGCAA 960

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DB 901 AATTGCTAGAGAAAAAAGATCTAGCGCGCGACGCTCTCTCCAGATAGCTCCCGCAA 960
QY 961 GAAATTCGCGCTGTAAACCAAGAAAGCGGAGAGGCGACCCCGGACGACGAAAGCAGCA 1020
DB 961 GAAATTCGCGCTGTAAACCAAGAAAGCGGAGAGGCGACCCCGGACGACGAAAGCAGCA 1020
QY 1021 AAGAAGGCCCTCCAGAAAGCTGCGAGAGACATGACGAGAGAGCTTGTGAGAAAT 1080
DB 1021 AAGAAGGCCCTCCAGAAAGCTGCGAGAGACATGACGAGAGAGCTTGTGAGAAAT 1080
QY 1081 CCGCGCCGCTCCCGCAAGACGAGAGTCCCGAGAGACGAGACGATGATCCCAAC 1140
DB 1081 CCGCGCCGCTCCCGCAAGACGAGAGTCCCGAGAGACGAGACGATGATCCCAAC 1140
QY 1141 TCGGATCTGACTATTACATGACATGCGCGCGGTGATCCGCTGAGAGAGACTATAA 1200
DB 1141 TCGGATCTGACTATTACATGACATGCGCGCGGTGATCCGCTGAGAGAGACTATAA 1200
QY 1201 AGTTCTAATGCGGCTCCAGATGCGGCGGCTGCTGAGCTGCGCGCTC 1260
DB 1201 AGTTCTAATGCGGCTCCAGATGCGGCGGCTGCTGAGCTGCGCGCTC 1260
QY 1261 GTGGGCGTACTGTTTGGAGCATCGTAAATGCGCGCTAGCTAA 1305
DB 1261 GTGGGCGTACTGTTTGGAGCATCGTAAATGCGCGCTAGCTAA 1305

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RESULT 4  
 AAC67867  
 ID AAC67867 standard; DNA; 1305 BP.

XX AAC67867;

XX 02-MAR-2001 (first entry)

DE Recombinant fowlpox virus-related polynucleotide, SEQ ID NO: 19.

XX Fowlpox virus; FPV; antiviral; antibacterial; vaccine;

KW Newcastle's disease; Marek's disease; infectious laryngotracheitis; ds.

OS Unidentified.

XX US6136318-A.

XX 24-OCT-2000.

PE 07-JUN-1995; 95US-0486414.

XX 26-FEB-1993; 93US-0024156.

PR 28-FEB-1994; 94WO-US02252.

XX (JUNK/) JUNKER D E.

PA (COCH/) COCHRAN M D.

XX Cochran MD, Junker DE;

XX WPI: 2000-686071/67.

PT New recombinant fowlpox virus useful as vaccines contains foreign DNA

XX inserted into specific non-essential region of the genome

XX Disclosure; Column 77-80; 56pp; English.

XX The present sequence is provided in a specification relating to a  
 CC recombinant fowlpox virus (FPV) that comprises a foreign DNA inserted  
 CC within a 3.5 kb EcoRI fragment of the FPV genomic DNA. The foreign DNA  
 CC can be expressed in host cells infected with FPV. The recombinant FPV  
 CC may be used in vaccines to protect animals (especially chickens) against  
 CC fowlpox and, depending on the source of the foreign DNA, other diseases,  
 CC particularly Newcastle's disease, Marek's disease or infectious  
 CC laryngotracheitis.

Sequence 1305 BP; 331 A; 349 C; 344 G; 281 T; 0 other;

Query Match 100.0%; Score 1305; DB 21; Length 1305;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGACCGCTCTCATCTGACAGGACACTGGCTTACTACGGGAAAGAGAGAGTGGTTAAC 60
DB 1 ATGACCGCTCTCATCTGACAGGACACTGGCTTACTACGGGAAAGAGAGAGTGGTTAAC 60
QY 61 AAACACATGATGATGCGGGAAGGAGGATGCTGACGCGGAGCTGATTCCTTTTC 120
DB 61 AAACACATGATGATGCGGGAAGGAGGATGCTGACGCGGAGCTGATTCCTTTTC 120
QY 121 TGGAGCTGTGTACAGATTAATCGGGAGCATATGCTTTGACCAAGCATATGACCGC 180
DB 121 TGGAGCTGTGTACAGATTAATCGGGAGCATATGCTTTGACCAAGCATATGACCGC 180
QY 181 CATTATATTTTGGAGAAATGCTTTTGGACATGCTACTGCTTCTCTCTGCTAGCCAG 240
DB 181 CATTATATTTTGGAGAAATGCTTTTGGACATGCTACTGCTTCTCTCTGCTAGCCAG 240
QY 241 AGCACCGCGCGCTGACAGTACATTTTAAAGCGGCGGCGCTGACGCGCTAAC 300
DB 241 AGCACCGCGCGCTGACAGTACATTTTAAAGCGGCGGCGCTGACGCGCTAAC 300
QY 301 ATACCGGCGGCTGGCGGCTATACAGATACCTACAGGATCAAGAGGCTGCGAGCTT 360
DB 301 ATACCGGCGGCTGGCGGCTATACAGATACCTACAGGATCAAGAGGCTGCGAGCTT 360
QY 361 GTGAGCTCAACCGGATTTTCAAGTGGAGACATGATATGAGGCGGCAAGAAAGAG 420
DB 361 GTGAGCTCAACCGGATTTTCAAGTGGAGACATGATATGAGGCGGCAAGAAAGAG 420
QY 421 AAGGGGGGCGCTTTGAGAGCGCTCGCTGCTGTTCTACGATTAAGGGGAGAGCGC 480
DB 421 AAGGGGGGCGCTTTGAGAGCGCTCGCTGCTGTTCTACGATTAAGGGGAGAGCGC 480
QY 481 GAGGACAAAGTCTGTCCAAATATAGAAAAGATACAGGAGATGCGGAGCTACAACTG 540
DB 481 GAGGACAAAGTCTGTCCAAATATAGAAAAGATACAGGAGATGCGGAGCTACAACTG 540
QY 541 CTATCTGAATGCGCGCTTCAATCTGCACAGATGTGGGAGGAGCTATGTTCTTAGCACC 600
DB 541 CTATCTGAATGCGCGCTTCAATCTGCACAGATGTGGGAGGAGCTATGTTCTTAGCACC 600
QY 601 CTTGTATCGGAAATGCGCGGAGCTGACTATATTTCTCCCACTGCTGCGCTCTGCGC 660
DB 601 CTTGTATCGGAAATGCGCGGAGCTGACTATATTTCTCCCACTGCTGCGCTCTGCGC 660
QY 661 CAATACTTGTGACCGCTGAAAATGCGAGATTTGCGCAACAGCTCTGCTACTCTAGAA 720
DB 661 CAATACTTGTGACCGCTGAAAATGCGAGATTTGCGCAACAGCTCTGCTACTCTAGAA 720
QY 721 GTTAAAGATGCGGAGTAACTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTT 780
DB 721 GTTAAAGATGCGGAGTAACTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTT 780
QY 781 ACAACAGACAGTATCAGACTGATTTCAAGGCGCAACACCTTTATCCGATGCGAGACCC 840
DB 781 ACAACAGACAGTATCAGACTGATTTCAAGGCGCAACACCTTTATCCGATGCGAGACCC 840
QY 841 AATACAGACAGCGGAGCGATATATCGGGGATACGAAAGATATTCGACGCGCTGGAAT 900
DB 841 AATACAGACAGCGGAGCGATATATCGGGGATACGAAAGATATTCGACGCGCTGGAAT 900
QY 901 AATTGCGAGGAAAGAAATCTAGGCGCGCAACCGCTGTCAGATAGGCTCCCGCAA 960
DB 901 AATTGCGAGGAAAGAAATCTAGGCGCGCAACCGCTGTCAGATAGGCTCCCGCAA 960
QY 961 GAAATTCGCGCTGTACCAAGGAGGCGGAGCGGAGCGGAGGAGGAGGAGGAGGAGG 1020
DB 961 GAAATTCGCGCTGTACCAAGGAGGAGGCGGAGCGGAGGAGGAGGAGGAGGAGGAGG 1020

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QY 1021 AAGAAAGCCCTCCAGAAAGCTCGGAGGACGACATGACAGGAGGCTTGTGAAAT 1080
DB 1021 AAGAAAGCCCTCCAGAAAGCTCGGAGGACGACATGACAGGAGGCTTGTGAAAT 1080
QY 1081 CCTGCGCGGCTCCCGGAAAGAGAGAGTCCCGGAGGAGGAGGAGGAGGAGGAGGAGG 1140
DB 1081 CCTGCGCGGCTCCCGGAAAGAGAGAGTCCCGGAGGAGGAGGAGGAGGAGGAGGAGG 1140
QY 1141 TCGGATCTGACTATTTACATGACATGCGCGCGCTGATCCCGGTGAGAGACTACTTAA 1200
DB 1141 TCGGATCTGACTATTTACATGACATGCGCGCGCTGATCCCGGTGAGAGACTACTTAA 1200
QY 1201 AGTTCTAATGCGGCTCCATGCTCCATATGCGGCGGCTTGTGAGGCTGCGGCGGCTC 1260
DB 1201 AGTTCTAATGCGGCTCCATGCTCCATATGCGGCGGCTTGTGAGGCTGCGGCGGCTC 1260
QY 1261 GTGGGCGTACTGTTTGGAGCATGTAAAGCGCGGCTAGCTTAA 1305
DB 1261 GTGGGCGTACTGTTTGGAGCATGTAAAGCGCGGCTAGCTTAA 1305

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RESULT 5  
 AAZ49300  
 ID AAZ49300 standard; cDNA; 1305 BP.  
 XX  
 AC AAZ49300;  
 DT 14-MAR-2000 (first entry)  
 XX  
 DE ILTV glycoprotein D (gp) gene.  
 XX  
 KW Fowlpox virus; FPV; recombinant; antigenic protein; expression;  
 KW Infectious laryngotracheitis virus; ILTV; Newcastle disease virus; NDV;  
 KW Marek's disease virus; cytokerin; promoter; homologous recombination;  
 KW homology vector; multivalent; live vaccine; glycoprotein D; ds.  
 OS Infectious laryngotracheitis virus.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..1305  
 FT /\*tag= a  
 FT /product= "Glycoprotein D (gp)"  
 XX  
 PN US6001369-A.  
 XX  
 PD 14-DEC-1999.  
 XX  
 PE 07-JUN-1995; 95US-0477459.  
 XX  
 PR 26-FEB-1993; 93US-0024156.  
 PR 28-FEB-1994; 94WO-US02252.  
 XX  
 PA (SVTR ) SYNPRO CORP.  
 XX  
 PI Junker DE, Cochran MD;  
 XX  
 DR WPI: 2000-071638/06.  
 DR P-PSDB: AAY58184.  
 XX  
 PT Recombinant fowlpox virus useful as a vaccine for immunizing fowl  
 PT against Marek's disease, Newcastle disease, Infectious  
 PT laryngotracheitis Virus and/or Fowlpox  
 XX  
 PS Claim 5; Columns 77-80; 56pp; English.  
 XX  
 CC The invention relates to a recombinant fowlpox virus (FPV)  
 CC comprising a foreign DNA inserted into a 4.2 kb EcoRI fragment  
 CC of the fowlpox virus genome. The foreign DNA is capable of being  
 CC expressed in a host cell into which the fowlpox virus has been  
 CC introduced and encodes an antigenic protein. The antigenic protein  
 CC which may be expressed includes infectious laryngotracheitis virus  
 CC (ILTV) glycoprotein B (gp) or glycoprotein D (gp). AAY58184, Newcastle  
 CC disease virus (NDV) haemagglutinin (HN, AAY58182) or fusion (F) protein

CC (AAV58183) and Marek's disease virus gB or gD. The foreign DNA may  
 CC alternatively encode a cytokine such as chicken myelomonocytic growth  
 CC factor (CMGF) or chicken interferon (cIFN). The foreign DNA in the  
 CC recombinant FPV is under the control of one or more synthetic pox  
 CC promoters, enabling control of strength and timing of heterologous  
 CC gene expression. The synthetic pox virus promoters that may be used are  
 CC based on promoters of the vaccinia virus and include early promoter 1  
 CC (EP1), late promoter 1 (LP1), EP2 and LP2 (AA49291-249294,  
 CC respectively). The recombinant FPV is generated via homologous  
 CC recombination between FPV DNA and a homology vector containing the  
 CC foreign DNA flanked by FPV sequences. The recombinant fowlpox viruses of  
 CC the invention are used as multivalent live vaccines for immunising fowl  
 CC against Marek's disease virus, NDV, ILTV and/or fowlpox virus. The  
 CC present sequence represents the ILTV glycoprotein D (gD) gene.  
 CC xx

Sequence 1305 BP; 331 A; 349 C; 344 G; 281 T; 0 other;

Query Match 100.0%; Score 1305; DB 21; Length 1305;  
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCACCGTCTCATCTCAGACGCGCTGCTACTACGGGAAGAGAGGCTCTTAC 60  
 Db 1 ATGCACCGTCTCATCTCAGACGCGCTGCTACTACGGGAAGAGAGGCTCTTAC 60  
 QY 61 AAACACATGATTCGGGTGGAAGAGGTGCTGCTCAGGCGCAGCTGATTCCTTTTC 120  
 Db 61 AAACACATGATTCGGGTGGAAGAGGTGCTGCTCAGGCGCAGCTGATTCCTTTTC 120  
 QY 121 TGGACTGTGTGACGATTATGCGGGAGCATATCGCTTTGTAGCAACGCTATGACCGC 180  
 Db 121 TGGACTGTGTGACGATTATGCGGGAGCATATCGCTTTGTAGCAACGCTATGACCGC 180  
 QY 181 CATTATTTTGAAGAAATGCTTTTGGACTATGCTACTGCTTTCTTCTCGCTAGCAG 240  
 Db 181 CATTATTTTGAAGAAATGCTTTTGGACTATGCTACTGCTTTCTTCTCGCTAGCAG 240  
 QY 241 AGCAGCGCGCGCTGACAGTACGACTATTTTAGCCGTGCGCGCTGACGCGCTAAC 300  
 Db 241 AGCAGCGCGCGCTGACAGTACGACTATTTTAGCCGTGCGCGCTGACGCGCTAAC 300  
 QY 301 ATACCGGCGGTGCGCGCTGATTAACAGATCCTACTAGGCTATCAGAGGCTGCGAGT 360  
 Db 301 ATACCGGCGGTGCGCGCTGATTAACAGATCCTACTAGGCTATCAGAGGCTGCGAGT 360  
 QY 361 GTGAGCTCAACCCGATTTCTAACTGTGAGCAGATGATGCGGCGCAAGAAAAGAG 420  
 Db 361 GTGAGCTCAACCCGATTTCTAACTGTGAGCAGATGATGCGGCGCAAGAAAAGAG 420  
 QY 421 AAGGGGGCGCTTTCGAGGCGCTCGTGTGCTGCTAGCTGATTAAGGCGAGCGCGC 480  
 Db 421 AAGGGGGCGCTTTCGAGGCGCTCGTGTGCTGCTAGCTGATTAAGGCGAGCGCGC 480  
 QY 481 GAGGACAGTACTGTCCAATCTATAGAAAAGATACAGGGAATGTGGCAGCTAAC 540  
 Db 481 GAGGACAGTACTGTCCAATCTATAGAAAAGATACAGGGAATGTGGCAGCTAAC 540  
 QY 541 CTATCTGAATGGCGGCTTAATCTGACAGATGTGGCGAGTACTATTTCTTACAC 600  
 Db 541 CTATCTGAATGGCGGCTTAATCTGACAGATGTGGCGAGTACTATTTCTTACAC 600  
 QY 601 CTGTATTCGGAATGGCGGCGAGTACTATATTTCTCCCAAGCTGCGCTCTGCGC 660  
 Db 601 CTGTATTCGGAATGGCGGCGAGTACTATATTTCTCCCAAGCTGCGCTCTGCGC 660  
 QY 661 CAATCTTCTGACCTGTAAGAAATCGGAGATTTGGCAAAACAGCTCTGTAACCTAGAA 720  
 Db 661 CAATCTTCTGACCTGTAAGAAATCGGAGATTTGGCAAAACAGCTCTGTAACCTAGAA 720  
 QY 721 GTTAAGATCGCTGTTTAAAGATCGGCTGCGAGCTTAACTTTTACCGTGAATGCTGG 780  
 Db 721 GTTAAGATCGCTGTTTAAAGATCGGCTGCGAGCTTAACTTTTACCGTGAATGCTGG 780

QY 781 ACAACAGACATATCAGACTGATTTCAAGGCGAACACCTTTATCCGATCGACACACC 840  
 Db 781 ACAACAGACATATCAGACTGATTTCAAGGCGAACACCTTTATCCGATCGACACACC 840  
 QY 841 AATACAGACACGCGGACGACATATTCGGGGATACGAGATTTTCTGACGCGCTGAAT 900  
 Db 841 AATACAGACACGCGGACGACATATTCGGGGATACGAGATTTTCTGACGCGCTGAAT 900  
 QY 901 AATTTGCTGAGAAAAGAAATCCTAGCGCGCAGACCTCTGTCAGATAGCGTCCGCAA 960  
 Db 901 AATTTGCTGAGAAAAGAAATCCTAGCGCGCAGACCTCTGTCAGATAGCGTCCGCAA 960  
 QY 961 GAAATTTCCGCTGTAAACCAAGAAAGCGGAGCGCACCCCGGACGCGCAGAAAGCAGAA 1020  
 Db 961 GAAATTTCCGCTGTAAACCAAGAAAGCGGAGCGCACCCCGGACGCGCAGAAAGCAGAA 1020  
 QY 1021 AAGAAGCGCCCTCAGAAAGCTGAGAGAGCAGATCGAGGCTCTGAGAGAAAT 1080  
 Db 1021 AAGAAGCGCCCTCAGAAAGCTGAGAGAGCAGATCGAGGCTCTGAGAGAAAT 1080  
 QY 1081 CCGCGCGCCCTCCGCAAGACGAGAAATCCCGAGAGACACCGACGATGATCAAC 1140  
 Db 1081 CCGCGCGCCCTCCGCAAGACGAGAAATCCCGAGAGACACCGACGATGATCAAC 1140  
 QY 1141 TCGATCTGACATATATGACATGATGCGCGCGCTGATCCGCTGAGAGAGCTACTAA 1200  
 Db 1141 TCGATCTGACATATATGACATGATGCGCGCGCTGATCCGCTGAGAGAGCTACTAA 1200  
 QY 1201 AGTTCTAATCCGCTCATATGCGCCATATTCGCGGGCTTGTGATGCGGCGTCCGCTC 1260  
 Db 1201 AGTTCTAATCCGCTCATATGCGCCATATTCGCGGGCTTGTGATGCGGCGTCCGCTC 1260  
 QY 1261 GTGGGCGCTACTGCTTTGAGAGCATCGTAATAATCGCGCGTACTAA 1305  
 Db 1261 GTGGGCGCTACTGCTTTGAGAGCATCGTAATAATCGCGCGTACTAA 1305

RESULT 6  
 AAT33504  
 ID AAT33504 standard; DNA; 13473 BP.  
 XX AAT33504;  
 AC 18-NOV-1996 (first entry)  
 DT  
 DE Infectious laryngotracheitis virus short region sequence.  
 XX Infectious laryngotracheitis virus; ILTV; herpesvirus;  
 KW attenuation; vector; vaccine; chicken; poultry; immunisation; ds.  
 XX Infectious laryngotracheitis virus.  
 OS  
 FH  
 FH Key location/Qualifiers  
 FT repeat\_region 1..273  
 FT /\*tag= a  
 FT /function= internal repeat region  
 FT misc\_feature 274..13371  
 FT /\*tag= b  
 FT /function= unique short sequence of ILTV  
 FT CDS complement (281..970)  
 FT /\*tag= c  
 FT /label= US2\_gene  
 FT 1059..2489  
 FT /\*tag= d  
 FT /label= Protein-kinase\_gene  
 FT 2575..4107  
 FT /\*tag= e  
 FT /label= UL47-1-like\_gene  
 FT 4113..4445  
 FT /\*tag= f  
 FT /label= ORF4  
 FT complement (4139..4519)  
 FT /\*tag= g

```

FT      /label= ORF4_reverse_complement
FT      misc_difference 4535
FT      /tag= h
FT      /note= "base 4535 is given as 's' in the
FT      specification"
FT      CDS
FT      4609..5487
FT      /tag= 1
FT      /label= g5_gene
FT      5697..8634
FT      /tag= 1
FT      /label= g60_gene
FT      complement (6948..7826)
FT      CDS
FT      /tag= k
FT      /label= ORF6_reverse_complement
FT      8462..9766
FT      /tag= 1
FT      /label= gD_gene
FT      9874..10962
FT      CDS
FT      /tag= m
FT      /label= gI_gene
FT      complement (10617..11150)
FT      CDS
FT      /tag= n
FT      /label= ORF8_reverse_complement
FT      11159..12658
FT      /tag= o
FT      /label= gE_gene
FT      12665..13447
FT      /tag= p
FT      /label= ORF10
FT      misc_difference 13002..13003
FT      /tag= q
FT      /note= "bases 13002-13003 are given as 'ss' in
FT      the specification"
FT      repeat_region
FT      13372..13473
FT      /tag= r
FT      /function= terminal repeat region
XX      W09508622-A1.
XX      30-MAR-1995.
XX      16-SEP-1994: 94MO-US10628.
XX      24-SEP-1993: 93US-0126597.
XX      (SYTR ) SYNPRO CORP.
XX      Cochran MD, Wild MA;
XX      PI
XX      WI: 1995-139591/18.
XX      DR P-PSDB: AAM00630, AAM00631, AAM00632, AAM00633, AAM00634, AAM00635,
XX      AAM00636, AAM00637, AAM00638, AAM00639, AAM00640, AAM00641 W00642.
XX      Recombinant attenuated infectious laryngotracheitis virus - for use
XX      in vaccines to protect poultry from infection from the virus, also
XX      methods of distinguishing between vaccinated and naturally infected
XX      birds
XX      Example 1: Page 79-94; 177pp: English.
XX      The unique short region (AAT33504) of infectious laryngotracheitis
XX      virus (ILTV) genomic DNA contains genes (see also AAT33505 and
XX      AAT33510-13) that are associated with ILTV virulence. A deletion in
XX      those genes, esp. the glycoprotein gG gene, glycoprotein gI gene,
XX      thymidine kinase gene, uS2 gene, uI47-like gene or the glycoprotein
XX      g60 gene, will attenuate the ILTV. A gene for a foreign antigen may
XX      be inserted into the uS2, uI47-like, ORF4, gG, g60 or gI gene to
XX      produce a recombinant ILTV. Recombinant ILTV may be used as a
XX      multivalent vaccine, esp. for use in poultry.
XX      Sequence 13473 BP; 3390 A; 3582 C; 3547 G; 2951 T; 3 other:
XX      Query Match 100.0%; Score 1305; DB 16; Length 13473;

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 ATGCACCGCTCTCATCTTCAGACGGCACTCGCGTACTACAGCGAAGAGAGAGGTGCTTAAC 60
DB      1 ATGCACCGCTCTCATCTTCAGACGGCACTCGCGTACTACAGCGAAGAGAGAGGTGCTTAAC 60
QY      8462 ATGCACCGCTCTCATCTTCAGACGGCACTCGCGTACTACAGCGAAGAGAGGTGCTTAAC 8521
DB      8462 ATGCACCGCTCTCATCTTCAGACGGCACTCGCGTACTACAGCGAAGAGAGGTGCTTAAC 8521
QY      61 AAACACATGATTTGCGGTGGAAAAAGGTGCTGCTCAGCGCGAGCTGTATTACCTTTTC 120
DB      8522 AAACACATGATTTGCGGTGGAAAAAGGTGCTGCTCAGCGCGAGCTGTATTACCTTTTC 8581
QY      121 TGCACTGTGTGACAGATTATCGGGAGCAATATCGCTTTTGACCAAGCATAGGACCG 180
DB      8582 TGCACTGTGTGACAGATTATCGGGAGCAATATCGCTTTTGACCAAGCATAGGACCG 8641
QY      181 CATTATTTTGGAGAAATGCTTTTGGACTATCGTACTGCTTCTTCCTTCGCTAGCCAG 240
DB      8642 CATTATTTTGGAGAAATGCTTTTGGACTATCGTACTGCTTCTTCCTTCGCTAGCCAG 8701
QY      241 AGCACCGCGCGCTGACGATGACGATACATTTTAAAGCGCGCGCTGACGCGCTAAC 300
DB      8702 AGCACCGCGCGCTGACGATGACGATACATTTTAAAGCGCGCGCTGACGCGCTAAC 8761
QY      301 ATACGGGGGGTGGCGCGGTAAACAGATACCTACTAGGGGTATCAAGAGCTGGAGCTT 360
DB      8762 ATACGGGGGGTGGCGCGGTAAACAGATACCTACTAGGGGTATCAAGAGCTGGAGCTT 8821
QY      361 GTGAGCTCAACCGATTTTCAAGTGGAGACATGATATCGCGCGCAAAAGAAAGAG 420
DB      8822 GTGAGCTCAACCGATTTTCAAGTGGAGACATGATATCGCGCGCAAAAGAAAGAG 8881
QY      421 AAGGGGGCGCTTTCGAGGCTCCGCTGCTGTTTACGTGATTAAGGCGAGCAGCGC 480
DB      8882 AAGGGGGCGCTTTCGAGGCTCCGCTGCTGTTTACGTGATTAAGGCGAGCAGCGC 8941
QY      481 GAGGACAAAGTACTGCTCAATCTATAGAAAGAGTACAGAGGAATGGCGAGCTACACTG 540
DB      8942 GAGGACAAAGTACTGCTCAATCTATAGAAAGAGTACAGAGGAATGGCGAGCTACACTG 9001
QY      541 CTATCTGAATGCGCGCTTCAATCTGACAGATGCGGAGTGGACTGCTATGTTCTAGCACC 600
DB      9002 CTATCTGAATGCGCGCTTCAATCTGACAGATGCGGAGTGGACTGCTATGTTCTAGCACC 9061
QY      601 CTGTATCGCGAAATGCGCGGAGCTGACTATATTTCCCCACGCTGCTGCTCTGCG 660
DB      9062 CTGTATCGCGAAATGCGCGGAGCTGACTATATTTCCCCACGCTGCTGCTCTGCG 9121
QY      661 CAATACTTGTGACCCCTGAAATCGGAGATTTGCGCAACAGCTCTGTACTCTAGAA 720
DB      9122 CAATACTTGTGACCCCTGAAATCGGAGATTTGCGCAACAGCTCTGTACTCTAGAA 9181
QY      721 GTTAAACGATGCTGTTTAAAGATCGGCTGACAGTAACTTTTACCGTGAATGCTGG 780
DB      9182 GTTAAACGATGCTGTTTAAAGATCGGCTGACAGTAACTTTTACCGTGAATGCTGG 9241
QY      781 ACAACAGACAGTATGACTGATTTCAAGCGCAACCTTTATTCGATCGACAGACC 840
DB      9242 ACAACAGACAGTATGACTGATTTCAAGCGCAACCTTTATTCGATCGACAGACC 9301
QY      841 AATACAGACAGCGGAGCGAGCTATATCGGGGATATGCAAAATATTCGACCGCTGGAAT 900
DB      9302 AATACAGACAGCGGAGCGAGCTATATCGGGGATATGCAAAATATTCGACCGCTGGAAT 9361
QY      901 AATTTGCTGAGAAAAAAGATCTAGCGCCCGACAGCCCTGTCAGATAGCTCCGCA 960
DB      9362 AATTTGCTGAGAAAAAAGATCTAGCGCCCGACAGCCCTGTCAGATAGCTCCGCA 9421
QY      961 GAAATTCGCCCTGTACCAAGAAAGCGGAGCGACCCCGGACGCAAGAACACAGGAA 1020
DB      9422 GAAATTCGCCCTGTACCAAGAAAGCGGAGCGGAGCGGACCCCGGACGCAAGAACACAGGAA 9481
QY      1021 AAGAGGGCGCTTCAGAGAGCTCGGAGGAGACATGAGGCAAGAGCTTGTGAGAAAT 1080
DB      1021 AAGAGGGCGCTTCAGAGAGCTCGGAGGAGACATGAGGCAAGAGCTTGTGAGAAAT 1080

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Accession	Sequence	Length
Dp 9482	AAGAAGGCCCTCCAGAAAGACTGGGAGACGACATCATGAGCCAGGCGTTCTTGAGAAANAT	9544
Qy 1081	CTCTCCGCGCTTCCCCGAGACGACGAGATGCCCGAGAGACCGGACGACGATGATCCAAAC	11440
Dp 9542	CCCTCCGCCCTCCCCGGAAGACGACGAAAGTCCCGGAGGACCCGAGACGATGATCCAAAC	9601
Qy 1141	TCGGATCCTGACATTTACATATGACATGACCGCCCGGTATCCCGGTGAGAGACTCTAA	1200
Dp 9602	TCGGATCCTGACATTTACATATGACATGACCGCCCGGTATCCCGGTGAGAGACTCTAA	9661
Qy 1201	AGTTCTATGCCGTTCTCATGCCCCATATTCGCGGCGTTTGTAAGCTGCGCGATCGCGCT	1260
Dp 9662	AGTTCTATGCCGTTCTCATGCCCCATATTCGCGGCGTTTGTAAGCTGCGCGATCGCGCT	9721
Qy 1261	GTGGGGCTACTGGTTGGGAGACATCGTAAATATGGCGCGTAGCTAA	1305
Dp 9722	GTGGGGCTACTGGTTGGGAGACATCGTAAATATGGCGCGTAGCTAA	9766

Result	ID	Accession	Location/Qualifiers
1	AA044384	standard; DNA; 13473 BP.	
2	AA044384;		
3	02-JUN-1997	(first entry)	
4	De	Infectious laryngotracheitis virus unique short region.	
5	Xx		
6	Xx		
7	Xx	ILT/ vaccine; vector: attenuation; poultry;	
8	KM	avian infectious bronchitis virus; Newcastle disease virus	
9	KM	infectious bursal disease virus of chickens;	
10	KM	Marek's disease virus; herpesvirus; ss.	
11	Xx		
12	Xx		
13	OS	Infectious laryngotracheitis virus USDA strain 8302.	
14	Key		
15	repeat_region	Location/Qualifiers	
16	FT	1..273	
17	FT	/*tag= a	
18	FT	274..13371	
19	FT	/*tag= b	
20	FT	/*note= "unique short region"	
21	FT	161..166	
22	FT	/*tag= c	
23	FT	/*note= "polyA signal for ORF1"	
24	FT	complement (281..970)	
25	FT	/*tag= d	
26	FT	/label= ORF1(RC)	
27	FT	/*note= "unique-like short 2 (US2) gene"	
28	FT	1007..1010	
29	FT	/*tag= e	
30	FT	/*note= "TATA signal for ORF1 and ORF2"	
31	FT	1040..1043	
32	FT	/*tag= f	
33	FT	/*note= "TATA signal for ORF1"	
34	FT	1042..1045	
35	FT	/*tag= g	
36	FT	/*note= "TATA signal for ORF2"	
37	FT	1059..2489	
38	FT	/*tag= h	
39	FT	/label= ORF2	
40	FT	/*note= "protein kinase gene"	
41	FT	2491..2496	
42	FT	/*tag= i	
43	FT	/*note= "polyA signal for ORF2"	
44	FT	2538..2543	
45	FT	/*tag= j	
46	FT	/*note= "polyA signal for ORF2"	
47	FT	2575..4107	
48	FT	/*tag= k	
49	FT	/label= ORF3	
50	FT	/*note= "unique long 47 (UL47)-like gene"	
51	FT	4523..4526	
52	TATA_signal		

FT	/*tag= 1
FT	/note="TATA signal for ORF4"
FT	4113..4445
FT	/*tag= m
FT	/label= ORF4
FT	complement (4139..4519)
FT	/*tag= n
FT	/label= ORF4(RC)
FT	4523..4526
FT	/*tag= o
FT	/note="TATA signal for ORF5"
FT	4609..5487
FT	/*tag= p
FT	/label= ORF5
FT	/note="glycoprotein gg gene"
FT	4609..4686
FT	/*tag= q
FT	4687..5484
FT	/*tag= i
FT	5564..5569
FT	/*tag= s
FT	/note="polyA site for ORF5"
FT	5653..5658
FT	/*tag= t
FT	/note="polyA signal for ORF5"
FT	5697..8654
FT	/*tag= u
FT	/label= ORF6
FT	/note="glycoprotein g60 gene"
FT	6987..7727
FT	/*tag= v
FT	/note="repeat region consists of approx. 23
FT	repeats of 30-36 bp"
FT	complement (6948..7826)
FT	/*tag= w
FT	/label= ORF6(RC)
FT	8455..8458
FT	/*tag= x
FT	/note="potential TATA signal for ORF7"
FT	8461..9766
FT	/*tag= y
FT	/label= ORF7
FT	/note="glycoprotein gd gene, alternative start
FT	codon at 8635..8635"
FT	9819..9822
FT	/*tag= z
FT	/note="TATA signal for ORF8"
FT	9874..10962
FT	/*tag= aa
FT	/label= ORF8
FT	/note="glycoprotein gi gene"
FT	9874..9939
FT	/*tag= ab
FT	9940..10959
FT	/*tag= ac
FT	complement (10617..11150)
FT	/*tag= ad
FT	/label= ORF8(RC)
FT	11069..11072
FT	/*tag= ae
FT	/note="TATA signal for ORF9"
FT	11159..12658
FT	/*tag= af
FT	/label= ORF9
FT	/note="glycoprotein gE gene"
FT	11159..11212
FT	/*tag= ag
FT	11213..12655
FT	/*tag= ah
FT	12483..12486
FT	/*tag= ai
FT	/note="TATA signal for ORF10"
FT	12665..13447
FT	

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FT      /*tag- a) /label- ORF10
FT      repeat_region 13572..13743
FT      /*tag- ak
PN      MO9629396-A1.
XX
XX      26-SEP-1996.
XX
XX      21-MAR-1996; 96WO-0503916.
XX
XX      06-JUN-1995; 95US-0468190.
PR      23-MAR-1995; 95US-0410121.
XX
XX      (SYTR ) SYNPRO CORP.
XX
XX      Cochran MD, Wild MA;
XX
XX      WPI: 1996-443172/44.
DR      P-PSDB; AAM06782;
DR      P-PSDB; AAM06783;
DR      P-PSDB; AAM06784;
DR      P-PSDB; AAM06785;
DR      P-PSDB; AAM06786;
DR      P-PSDB; AAM06787;
DR      P-PSDB; AAM06788;
DR      P-PSDB; AAM06789;
DR      P-PSDB; AAM06790;
DR      P-PSDB; AAM06791;
DR      P-PSDB; AAM06792;
DR      P-PSDB; AAM06793.
XX
XX      Recombinant infectious laryngotracheitis virus with deletion in the
PT      glycoprotein G, gI or US2 gene, etc. - useful for vaccines against
PT      infectious laryngotracheitis in poultry
XX
XX      Example 11; Page 88-103; 216pp; English.
XX
XX      The nucleotide sequence of 13,473 bp of contiguous DNA (AAT44384)
CC      from the unique short region of infectious laryngotracheitis virus
CC      (ILTV) contains the entire 13,098 bp unique short region and
CC      includes 13 open reading frames that encode proteins (AAM06782-94) of
CC      over 100 amino acids, 8 of which show significant homology to other
CC      virus genes. Novel recombinant, attenuated ILTV comprises the ILTV
CC      genome contg. a deletion in the unique short region, esp. in the
CC      glycoprotein gE, gI, US2, ORF4, UL47-like or g60 gene. The
CC      attenuated virus is useful as a vaccine against ILTV. A foreign
CC      gene encoding an antigen e.g. from another avian virus can be
CC      inserted into the US2, UL47-like, ORF4, gE, g60 or gI gene to
CC      provide a multivalent vaccine for chickens and other poultry.
CC      Deletion of the gE or gI gene provides as a negative marker to
CC      distinguish vaccinated from infected animals.
XX
XX      Sequence 13473 BP; 3390 A; 3581 C; 3547 G; 2952 T; 3 other;
SQ
Query Match      100.0%; Score 1305; DB 17; Length 13473;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      8642 CATTATTTTGGAGAAATGCTTTTGGACTATGCTACTGCTTCTTCCTTCCGCTAACCG 8701
QY      AGACACCGCCGCGCTACAGTACGACTACATTTTAAAGCCGTCGCGCTGACGCGCTAAC 300
Db      8702 AGCACCCGCGCGCTACAGTACGACTACATTTTAAAGCCGTCGCGCTGACGCGCTAAC 8761
QY      ATACCGCGCGCTTGGCCGCTATTAACAGATACCTCACTAGGGATATTAAGAGCTGGACGTT 360
Db      8762 ATACCGCGCGCTTGGCCGCTATTAACAGATACCTCACTAGGGATATTAAGAGCTGGACGTT 8821
QY      GTCGAGCTCAACCGATTTTCAAGTGGACGACATGATATGCGCGCCAAAGAAAGAG 420
Db      8822 GTCGAGCTCAACCGATTTTCAAGTGGACGACATGATATGCGCGCCAAAGAAAGAG 8881
QY      AAGGGGGCCCTTTGAGAGCCCTCCGTCGTGTTCTACGTATTAAGGCGAGCAGCGC 480
Db      8882 AAGGGGGCCCTTTGAGAGCCCTCCGTCGTGTTCTACGTATTAAGGCGAGCAGCGC 8941
QY      GAGGACAGTACTGCTCCATCTATAGAAAGAGTACAGGGAATGGCGACGTACAACTG 540
Db      8942 GAGGACAGTACTGCTCCATCTATAGAAAGAGTACAGGGAATGGCGACGTACAACTG 9001
QY      CTATCTGAATGCGCGCGCTTCAATCTGACAGATGTTGGGACGTATGTTCTTACGACC 600
Db      9002 CTATCTGAATGCGCGCGCTTCAATCTGACAGATGTTGGGACGTATGTTCTTACGACC 9061
QY      CTTGATATCGGAAATGCGCGCGGACTGACTATATTTCCCCACCTGCTGCGCTCTGCG 660
Db      9062 CTTGATATCGGAAATGCGCGCGGACTGACTATATTTCCCCACCTGCTGCGCTCTGCG 9121
QY      CAATACTGCTGACCCCGTAAATGCGGAGATTTGCGCAACAGCTCTGCTACTGAA 720
Db      9122 CAATACTGCTGACCCCGTAAATGCGGAGATTTGCGCAACAGCTCTGCTACTGAA 9181
QY      GTTACGATGCGCTTTTAAAGATGCGGCTGCTGCTTACTTTTACCGTGAATGCTGG 780
Db      9182 GTTACGATGCGCTTTTAAAGATGCGGCTGCTGCTTACTTTTACCGTGAATGCTGG 9241
QY      ACAACAGACAGTATGACTGATTTCAAGCGCAACCTTTATCCGATGCGACACC 840
Db      9242 ACAACAGACAGTATGACTGATTTCAAGCGCAACCTTTATCCGATGCGACACC 9301
QY      AATACAGACAGCGGAGCGAGATATCGGGGATACGAATATTCGACGCGTGAAT 900
Db      9302 AATACAGACAGCGGAGCGAGATATCGGGGATACGAATATTCGACGCGTGAAT 9361
QY      AATTGCTGAGAAAGAAATTCCTAGCGCGCCAGACCTCTGCTCAGATACGTCGCGCA 960
Db      9362 AATTGCTGAGAAAGAAATTCCTAGCGCGCCAGACCTCTGCTCAGATACGTCGCGCA 9421
QY      GAAATTCGCCCTGTATACCAAGAAAGCGGAGGCGCACCCCGGAGCAAGAACAGCGAA 9481
Db      9422 GAAATTCGCCCTGTATACCAAGAAAGCGGAGGCGCACCCCGGAGCAAGAACAGCGAA 9481
QY      AAGAGGCGCCCTCCAGAGACTGAGAGAGACATGACGAGCGAGGCTTTGGGAAAT 1080
Db      9482 AAGAGGCGCCCTCCAGAGACTGAGAGAGACATGAGAGCGAGGCTTTGGGAAAT 9541
QY      CTTGCGCCCTCCCTCCGGAAGAGAGAGTCCCGAGAGACCGAGACGATGATCCAAAC 1140
Db      9542 CTTGCGCCCTCCCTCCGGAAGAGAGAGTCCCGAGAGACCGAGACGATGATCCAAAC 9601
QY      TCGGATCTGACTATTAATGACATGCGCGCGTATCCCGGTGAGAGACTACTAA 1200
Db      9602 TCGGATCTGACTATTAATGACATGCGCGCGTATCCCGGTGAGAGACTACTAA 9661
QY      AGTTCTAATGCGCTTCATGATGACATGATGCGCGCGTATCCCGGTGAGAGACTACTAA 1260
Db      9662 AGTTCTAATGCGCTTCATGATGACATGATGCGCGCGTATCCCGGTGAGAGACTACTAA 9721
QY      GTGGGGCTACTGTTTGGAGACATGTAATGCGCGGTGACTAA 1305
Db      9722 GTGGGGCTACTGTTTGGAGACATGTAATGCGCGGTGACTAA 9766
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RESULT 8
ID AAT44385
XX AAT44385 standard; DNA: 18912 BP.
AC AAT44385;
XX
DT 02-JUN-1997 (first entry)
XX
DE Infectious laryngotracheitis virus unique short + flanking region.
XX
KW ILTV; vaccine; vector: attenuation; poultry;
KW avian infectious bronchitis virus; Newcastle disease virus;
KW infectious bursal disease virus of chickens;
KW Marek's disease virus; herpesvirus; ss.
XX
OS Infectious laryngotracheitis virus USDA strain 8302.
XX
FH Key Location/Qualifiers
FT repeat_region 1..2909
FT /*tag= a
FT /note= "short repeat region"
FT 697..1533
FT /*tag= b
FT /label= "SRORF2"
FT /note= "US10 gene"
FT complement (2916..3605)
FT /*tag= c
FT /label= "SRORF1"
FT /note= "short repeat open reading frame 1"
FT 2910..16003
FT /*tag= d
FT /note= "unique short region"
FT 2796..2891
FT /*tag= e
FT /note= "polyA signal for ORF1"
FT complement (2916..3605)
FT /*tag= f
FT /label= "ORF1(RC)"
FT /note= "unique-like short 2 (US2) gene"
FT 3642..3645
FT /*tag= g
FT /note= "TATA signal for ORF1 and ORF2"
FT 3675..3678
FT /*tag= h
FT /note= "TATA signal for ORF1"
FT 3677..3680
FT /*tag= i
FT /note= "TATA signal for ORF2"
FT 3694..5124
FT /*tag= j
FT /label= "ORF2"
FT /note= "protein kinase gene"
FT 5126..5131
FT /*tag= k
FT /note= "polyA signal for ORF2"
FT 5173..5178
FT /*tag= l
FT /note= "polyA signal for ORF2"
FT 5210..7081
FT /*tag= m
FT /label= "ORF3"
FT /note= "unique long 47 (ULA7)-like gene"
FT 7158..7161
FT /*tag= n
FT /note= "TATA signal for ORF4"
FT 6748..7080
FT /*tag= o
FT /label= "ORF4"
FT complement (6774..7154)
FT /*tag= p
FT /label= "ORF4(RC)"

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FT TATA_signal 7158..7161
FT /*tag= q
FT /note= "TATA signal for ORF5"
FT 7245..8123
FT /*tag= r
FT /label= "ORF5"
FT /note= "glycoprotein g6 gene"
FT 7245..7322
FT /*tag= s
FT 7323..8120
FT /*tag= t
FT 8200..8205
FT /*tag= u
FT /note= "polyA site for ORF5"
FT 8289..8294
FT /*tag= v
FT /note= "polyA signal for ORF5"
FT 8333..11290
FT /*tag= w
FT /label= "ORF6"
FT /note= "glycoprotein g60 gene"
FT 9623..10363
FT /*tag= x
FT /note= "repeat region consists of approx. 23
FT repeats of 30-36 bp"
FT complement (9584..10462)
FT /*tag= y
FT /label= "ORF6(RC)"
FT 11091..11094
FT /*tag= z
FT /note= "potential TATA signal for ORF7"
FT 11098..12402
FT /*tag= aa
FT /label= "ORF7"
FT 12455..12448
FT /*tag= ab
FT /note= "TATA signal for ORF8"
FT 12510..13598
FT /*tag= ac
FT /label= "ORF8"
FT /note= "glycoprotein gi gene"
FT 12510..12575
FT /*tag= ad
FT 12576..13595
FT /*tag= ae
FT complement (13253..13786)
FT /*tag= af
FT /label= "ORF8(RC)"
FT 13705..13708
FT /*tag= ag
FT /note= "TATA signal for ORF9"
FT 13792..15291
FT /*tag= ah
FT /label= "ORF9"
FT /note= "glycoprotein gE gene"
FT 13792..13845
FT /*tag= ai
FT 13846..15288
FT /*tag= aj
FT 15116..15119
FT /*tag= ak
FT /note= "TATA signal for ORF10"
FT 15298..16080
FT /*tag= al
FT /label= "ORF10"
FT 16004..18912
FT /*tag= am
FT 16129..17013
FT /*tag= an
FT complement (17380..18216)
FT /*tag= ao
XX PN WO9629396-A1.

```



XX 26-SEP-1996.  
 PD 26-SEP-1996.  
 XX 21-MAR-1996; 96MO-US03916.  
 PF 21-MAR-1996; 96MO-US03916.  
 PR 06-JUN-1995; 95US-0468190.  
 PR 23-MAR-1995; 95US-0410121.  
 XX (SYTR ) SYNTRO CORP.  
 FA (SYTR ) SYNTRO CORP.  
 XX Cochran MD, Wild MA;  
 PI Cochran MD, Wild MA;  
 XX WPI: 1996-443172/44.  
 DR P-PSDS: AAM06782, AAM06783, AAM06784, AAM06785, AAM06786, AAM06787,  
 DR AAM06788, AAM06789, AAM06790, AAM06791, AAM06792, AAM06793, AAM01415,  
 DR AAM01416.  
 XX Recombinant infectious laryngotracheitis virus with deletion in the  
 PT glycoprotein G, gI or uS2 gene, etc. - useful for vaccines against  
 PT infectious laryngotracheitis in poultry  
 XX  
 PS Example 11; Page 138-154; 216pp; English.  
 XX  
 CC The nucleotide sequence of 19,912 bp of contiguous DNA (AAT44385)  
 CC from the unique short and flanking region of infectious  
 CC laryngotracheitis virus (ILTV) contains the entire 13,098 bp unique  
 CC short region (see also AAT44384) and includes 17 open reading frames  
 CC that encode proteins (AAM06782-94, AAM01415-16) of over 100 amino  
 CC acids, 10 of which show homology to other virus genes. Novel  
 CC recombinant, attenuated ILTV comprises the ILTV genome contg. a  
 CC deletion in the unique short region, esp. in the glycoprotein gS,  
 CC gI, uS2, ORF4, UL47-like or g60 gene. The attenuated virus is  
 CC useful as a vaccine against ILTV. A foreign gene encoding an  
 CC antigen e.g. from another avian virus can be inserted into the uS2,  
 CC UL47-like, ORF4, gS, g60 or gI gene to provide a multivalent  
 CC vaccine for chickens and other poultry. Deletion of the gS or gI  
 CC gene provides as a negative marker to distinguish vaccinated from  
 CC infected animals.  
 XX  
 SQ Sequence 18912 BP; 4416 A; 5261 C; 5251 G; 3984 T; 0 other;  
 Query Match 100.0%; Score 1305; DB 17; Length 18912;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACCGCTCTCATCTCAGACGCGACTGCGCTTACTACGCGAAGAGAGGCTGTAC 60  
 DB 11098 ATGACCGCTCTCATCTCAGACGCGACTGCGCTTACTACGCGAAGAGAGGCTGTAC 11357  
 QY 61 AAACACATGATGCGGTGGGAAAGCGGTGCTGACGCGAGCGATGATTCCTTTTC 120  
 DB 11158 AAACACATGATGCGGTGGGAAAGCGGTGCTGACGCGAGCGATGATTCCTTTTC 11217  
 QY 121 TGGACTTGTCTCAGGATATGCGGAGCATATCTGCTTTGACGCAACGCTATGAGACCGC 180  
 DB 11218 TGGACTTGTCTCAGGATATGCGGAGCATATCTGCTTTGACGCAACGCTATGAGACCGC 11277  
 QY 181 CATTTATTTTGGAGAAATGCTTTTGGACTATGCTACTGCTTTCTCTTCTGCTAGCCAG 240  
 DB 11278 CATTTATTTTGGAGAAATGCTTTTGGACTATGCTACTGCTTTCTCTTCTGCTAGCCAG 11337  
 QY 241 AGCACCGCGCGCTGACGATGACATACATTTAGGCGCTGCGCGCTGACGCGCTAACG 300  
 DB 11338 AGCACCGCGCGCTGACGATGACATACATTTAGGCGCTGCGCGCTGACGCGCTAACG 11397  
 QY 301 ATACCGCGGCTTGGCCGCTATACAGATACCTCACTAGGATATCAAGAGGCTGCGACGTT 360  
 DB 11398 ATACCGCGGCTTGGCCGCTATACAGATACCTCACTAGGATATCAAGAGGCTGCGACGTT 11457  
 QY 361 GTGAGCTCAACCGGATTTCTAACGTGGAGACATGATATGCGGCGCAAGAAAAGAG 420  
 DB 11458 GTGAGCTCAACCGGATTTCTAACGTGGAGACATGATATGCGGCGCAAGAAAAGAG 11517

QY 421 AAGGGGGCCCTTTCGAGGCGCTCGCTGCTTCTACGATTAAGGGGCGAGACGGC 480  
 DB 11518 AAGGGGGCCCTTTCGAGGCGCTCGCTGCTTCTACGATTAAGGGGCGAGACGGC 11577  
 QY 481 GAGGACAGTACTGCTCAGTCTATAGAAAAGATACAGGAGATGCGGACGTAACATG 540  
 DB 11578 GAGGACAGTACTGCTCAGTCTATAGAAAAGATACAGGAGATGCGGACGTAACATG 11637  
 QY 541 CTATCTGAATGCGCGCTTCAATCTGCACAGATGTCGAGTGTGACTATGTTCTGACAC 600  
 DB 11638 CTATCTGAATGCGCGCTTCAATCTGCACAGATGTCGAGTGTGACTATGTTCTGACAC 11697  
 QY 601 CTTGATGCGCAATAGCGCGGAGCTGACTATATTCCTCCACCTGCGGCGCTCTGCGC 660  
 DB 11698 CTTGATGCGCAATAGCGCGGAGCTGACTATATTCCTCCACCTGCGGCGCTCTGCGC 11757  
 QY 661 CAATCTGCTGACCCCTGAAATGCGGAGATTTTGGCAACAGCTCTGTAACCTAGAA 720  
 DB 11758 CAATCTGCTGACCCCTGAAATGCGGAGATTTTGGCAACAGCTCTGTAACCTAGAA 11817  
 QY 721 GTTAACGATCGCTGTTTAAAGTGGGTCGACGCTTAACCTTTTACCGTCAAAATGCTGG 780  
 DB 11818 GTTAACGATCGCTGTTTAAAGTGGGTCGACGCTTAACCTTTTACCGTCAAAATGCTGG 11877  
 QY 781 ACAACAGACAGTATCAGACTGATTTTCAAGGCGAACCTTTTATCCGATGCGACACAC 840  
 DB 11878 ACAACAGACAGTATCAGACTGATTTTCAAGGCGAACCTTTTATCCGATGCGACACAC 11937  
 QY 841 AATACACGACAGCGCGAGCAGATATATGCGGATATGCAAGATATTTGACGCGTGAAT 900  
 DB 11938 AATACACGACAGCGCGAGCAGATATATGCGGATATGCAAGATATTTGACGCGTGAAT 11997  
 QY 901 AATTGCTGAGAGAAAAGAAATCTTAGCGCCGACAGACCTCTCCAGATAGCTCCGCA 960  
 DB 11998 AATTGCTGAGAGAAAAGAAATCTTAGCGCCGACAGACCTCTCCAGATAGGTCGCGCA 12057  
 QY 961 GAAATTCCTCGCTGTAAACAAAGGAGGAGGCGCACCCGCGAGCGCAAGAAAGACGCA 1020  
 DB 12058 GAAATTCCTCGCTGTAAACAAAGGAGGAGGCGCACCCGCGAGCGCAAGAAAGACGCA 12117  
 QY 1021 AAGAAAGCCCTCCAGAAAGTCCGAGAGCAGATGACAGGAGAGGCTTCTGAGAAAT 1080  
 DB 12118 AAGAAAGCCCTCCAGAAAGTCCGAGAGCAGATGACAGGAGAGGCTTCTGAGAAAT 12177  
 QY 1081 CCTGCGGCGCTCCCGAAGAGAGAGAAATCCCCGAGAGACACCGACAGATATCCAAAC 1140  
 DB 12178 CCTGCGGCGCTCCCGAAGAGAGAGAAATCCCCGAGAGACACCGACAGATATCCAAAC 12237  
 QY 1141 TCGGATCCTGACTATTAACAATGACATGCGCGCGCTGATCCGCTGAGAGACATCTAA 1200  
 DB 12238 TCGGATCCTGACTATTAACAATGACATGCGCGCGCTGATCCGCTGAGAGACATCTAA 12297  
 QY 1201 AGTTCTAATGCGCTGTCATGCCCATATTCGCGCGCTTCTGACCTGCGCGCTC 1260  
 DB 12298 AGTTCTAATGCGCTGTCATGCCCATATTCGCGCGCTTCTGACCTGCGCGCTC 12357  
 QY 1261 GTGGGCGTACTAGCTTTGAGAGCATGTAATAAGCGCGCTACTAA 1305  
 DB 12358 GTGGGCGTACTAGCTTTGAGAGCATGTAATAAGCGCGCTACTAA 12402

RESULT 9  
 AAQ22986  
 ID AAQ22986 standard; DNA; 3502 BP.  
 XX  
 AC AAQ22986;  
 XX  
 DT 02-NOV-1992 (first entry)  
 XX  
 DE Sequence of ILTV gp60 gene.  
 XX  
 KW Subunit vaccine; immunogen; glycoprotein; promoter; ss.  
 XX

OS Infectious laryngotracheitis virus.  
 XX Key Location/Qualifiers  
 FT TATN\_signal 294..299  
 FT /tag= a  
 FT 339..3326  
 FT repeat\_unit 1692..1712  
 FT /tag= b  
 FT repeat\_unit 1755..1775  
 FT /tag= c  
 FT repeat\_unit 1824..1841  
 FT /tag= d  
 FT repeat\_unit 1857..1871  
 FT /tag= e  
 FT repeat\_unit 1923..1943  
 FT /tag= f  
 FT repeat\_unit 1986..2006  
 FT /tag= g  
 FT repeat\_unit 2019..2039  
 FT /tag= h  
 FT repeat\_unit 2115..2129  
 FT /tag= i  
 FT repeat\_unit 2178..2198  
 FT /tag= j  
 FT repeat\_unit 2211..2228  
 FT /tag= k  
 FT repeat\_unit 2241..2261  
 FT /tag= l  
 FT repeat\_unit 2304..2324  
 FT /tag= m  
 FT repeat\_unit 2334..2351  
 FT /tag= n  
 FT repeat\_unit 2351  
 FT /tag= o  
 XX MO9203554-A.  
 XX PN  
 XX 05-MAR-1992.  
 XX PD  
 XX 23-AUG-1991; 91WO-AU00383.  
 XX PF  
 XX 24-AUG-1990; 90AU-0001937.  
 XX PR  
 XX (WEBS-) WEBSTER A PTY LTD.  
 XX PA  
 XX Sheppard MG, Prieaux C, Johnson M, Fahey KJ, York JJ;  
 XX PI Kongsuwan K;  
 XX P-PSDB; AAR22234.  
 XX DR  
 XX MPI: 1992-096898/12.  
 XX PT  
 XX Vaccines against ILTV for use in chickens - comprises  
 PT non-infectious sub-units or live recombinant viruses and may be  
 PT administered by aerosol  
 XX  
 XX Claim 14; Fig 6; 122pp; English.  
 XX  
 CC The inventors claim a non-infectious subunit vaccine for use against  
 CC ILTV which comprises a glycoprotein of ILTV. They also claim DNA  
 CC encoding the vaccine, a synthetic polypeptide displaying the  
 CC antigenicity of the 205k complex or 60k ILTV glycoprotein and a  
 CC recombinant ILTV with heterologous DNA inserted into a non-essential  
 CC region of the genome; and a recombinant DNA mol. comprising an ILTV  
 CC promoter region operatively linked to a heterologous DNA sequence.  
 CC The promoter region is the ILTV gp60 promoter, gp205 (gpB) promoter  
 CC or the ORF3 promoter region. Kpnk/ORF3 is located 5' of the gp60  
 CC gene. The deduced AA sequence of the gp60 gene has 19 hydrophobic  
 CC AA residues at the N-terminus which may correspond to the signal  
 CC sequence. A second region of hydrophobic AAs (posn. 960 to 989) at  
 CC the C-terminus could function as a transmembrane anchor sequence.  
 CC There are nine potential N-linked glycosylation sites on the ILTV  
 CC gp60 protein. One of these sites at residue 677, may not be active  
 CC due to the presence of a proline residue within the N-X-S/T signal.  
 CC There are repeated sequences within the ILTV gp60 coding region.

CC They are not perfectly conserved but several copies had diverged so  
 CC that only 4 AAs out of 7 were conserved in all 13 copies of the  
 CC repeats. There is no significant homology between the protein and  
 CC any sequenced herpesvirus proteins in the database called PIR.  
 XX  
 SO Sequence 3502 BP; 845 A; 969 C; 920 G; 768 T; 0 other;  
 Query Match 27.7%; Score 361; DB 13; Length 3502;  
 Best Local Similarity 98.6%; Pred. No. 2.1e-104;  
 Matches 364; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 ATGCACGGTCTCTCATCTCAGACGGCAGTCCGCTTACTACCGGAAAGAGGCTTTAAC 60  
 DB 3134 ATGCACGGTCTCTCATCTCAGACGGCAGTCCGCTTACTACCGGAAAGAGGCTTTAAC 3193  
 QY 61 AATCAGATGATTCGGGTGGAACAGCGTGTCTCAGCGCCAGCTGATTCACCTTTTC 120  
 DB 3194 GAACACATGATTCGGGTGGAACAGCGTGTCTCAGCGCCAGCTGATTCACCTTTTC 3253  
 QY 121 TGGACTTGTGTCAAGATTATGCGGAGCAATATCTGCTTTGACGCAACGCTATGACCGC 180  
 DB 3254 TGGACTTGTGTCAAGATTATGCGGAGCAATATCTGCTTTGACGCAACGCTATGACCGC 3313  
 QY 181 CATTTATTTTGAAGAAATGCTTTTGGACTATGCTACTGCTTCTTCTTCTGCTACCGAG 240  
 DB 3314 CATTTATTTTGAAGAAATGCTTTTGGACTATGCTACTGCTTCTTCTTCTGCTACCGAG 3373  
 QY 241 AGCAGCGCCCGCTCAGTACGACTACATTTTATGCGCGCGCTGACGCGCTAACCC 300  
 DB 3374 AGCAGCGCCCGCTCAGTACGACTACATTTTATGCGCGCGCTGACGCGCTAACCC 3433  
 QY 301 ATACCGGGGTTGGCCCGTTATACATATCTACTAGGGTATCAAGAGCTGCGACTT 360  
 DB 3434 ATACCGGGGTTGGCCCGTTATACATATCTACTAGGGTATCAAGAGCTGCGACTT 3493  
 QY 361 GTGAGCTC 369  
 DB 3494 GTGAGCTC 3502  
 RESULT 10  
 AAT44399  
 ID AAT44399 standard; DNA; 42 BP.  
 XX  
 AC AAT44399;  
 XX  
 DT 03-JUN-1997 (first entry)  
 XX  
 DE Homology vector 562-61.1F junction B.  
 XX  
 KW ILTV; vaccine; homology vector 562-61.1F; attenuation; poultry;  
 KW avian infectious bronchitis virus; Newcastle disease virus;  
 KW infectious bursal disease virus of chickens;  
 KW Marek's disease virus; herpesvirus; glycoprotein gI; ss.  
 XX  
 OS Chimeric infectious laryngotracheitis virus.  
 XX  
 XX Key Location/Qualifiers  
 FT misc\_RNA 1..24  
 FT /tag= a  
 FT /label= ILTV  
 FT /note= "3' end of approx. 1619 bp Asp718I-XbaI  
 FT subfragment of the ILTV 8.0 kb Asp718I  
 FT fragment"  
 FT misc\_RNA 19..42  
 FT /tag= b  
 FT /label= ILTV  
 FT /note= "5' end of approx. 691 bp XbaI-XhoI fragment  
 FT of ILTV, generated by PCR"  
 XX  
 XX MO9629396-A1.  
 XX 26-SEP-1996.  
 PD

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XX 21-MAR-1996; 96WO-US03916.
PF 06-JUN-1995; 95US-0468190.
PR 23-MAR-1995; 95US-0410121.
XX (SYTR ) SYNPRO CORP.
PA Cochran MD, Wild MA;
PI WPI: 1996-443172/44.
XX Recombinant infectious laryngotracheitis virus with deletion in the
PT glycoprotein G, gI or uS2 gene, etc. - useful for vaccines against
PT infectious laryngotracheitis in poultry
XX
XX Example 4; Fig 7B; 216pp; English.
XX
CC Junction sequences (AA144398-403) are provided of the DNA fragments
CC used to construct homology vector 562-61.1P, a plasmid designed for
CC the purpose of deleting a 983 bp portion of the glycoprotein gI
CC gene from the unique short region (see also AA144384) of infectious
CC laryngotracheitis virus (ILT), and replacing it with uida DNA.
CC The vector incorporates a screenable marker, the E. coli uida gene,
CC flanked by ILTV DNA. The homology vector is used to construct
CC attenuated ILTV S-ILT-011, which is useful as a killed vaccine to
CC protect chickens from ILT disease and as a negative marker to
CC distinguish vaccinated from infected animals. It is also used to
CC construct S-ILT-013, which also has a deletion in the gC gene.
XX
SQ Sequence 42 BP; 12 A; 11 C; 8 G; 11 T; 0 other;
Query Match 3.2%; Score 42; DB 17; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 695 CGCAACAGCTCTGTAAGTTCAGATGCGCTGT 736
Db 1 CGCAACAGCTCTGTAAGTTCAGATGCGCTGT 42
RESULT 11
AAQ21833
ID AAQ21833 standard; DNA; 390 BP.
XX
AC AAQ21833;
XX
DT 08-JUN-1992 (first entry)
DE Randomising oligonucleotide used in SPERT mRNA prepn.
XX
KW Systematic polypeptide evolution by reverse translation; SPERT;
KW ligand binding; ss.
XX
OS Synthetic.
XX
FN WO9202536-A.
PD 20-FEB-1992.
XX
PF 01-AUG-1991; 91WO-US05463.
PR 02-AUG-1990; 90US-0561968.
XX
PA (COLS ) UNIV OF COLORADO.
XX
PI Gold L, Tuerc C;
DR WPI: 1992-080018/10.
XX
PT New method of systematic polypeptide evolution by reverse
PT translation - by linking each polypeptide in sample mixt. to
PT individualised mRNA allowing further synthesis of selected

```

```

PT polypeptide(s)
XX
PS Example; Page 55; 102pp; English.
XX
CC The sequence is that of an example randomising oligonucleotide which
CC is used in the prepn. of mRNA encoding candidate polypeptides for the
CC method of systematic polypeptide evolution by reverse translation
CC (SPERT). The method provides a rapid way of isolating and identifying
CC polypeptide ligands which bind to target mols. The polypeptide ligands
CC can be used in e.g. assay methods, diagnostic procedures, cell sorting,
CC as activators or inhibitors of target mol. function, as probes, as
CC sequestering agents, drug delivery vehicles, modifiers of hormone
CC action and as catalysts. See also AAQ21830-Q21832.
XX
SQ Sequence 390 BP; 125 A; 126 C; 133 G; 6 T; 0 other;
Query Match 3.2%; Score 41.6; DB 13; Length 390;
Best Local Similarity 51.6%; Pred. No. 0.011;
Matches 95; Conservative 0; Mismatches 89; Indels 0; Gaps 0;
QY 1003 GACGACGAAAGCAGGAAAGAGCCCTCCAGAACTCGAGAGAGCATGCAGCA 1062
Db 201 GACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 260
QY 1063 GAGGCTTGTGGAGAAATCTGCGCCCTCCGGAAGAGCAAGTCCCGAGACAC 1122
Db 261 GACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 320
QY 1123 GAGCAGATGATCCAAACTCGATCTGACTATTACATGACATGCCCGGTATCCG 1182
Db 321 GACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 380
QY 1183 GTGG 1186
Db 381 ATGG 384
RESULT 12
AAQ36859
ID AAQ36859 standard; DNA; 390 BP.
XX
AC AAQ36859;
XX
DT 22-JUN-1993 (first entry)
DE PCR primer for 5' fixed sequence contg. T7 promoter and RBS.
XX
KW Systematic peptide evolution by reverse translation; SPERT; ligand;
KW specific; inhibitors; probes; assay; cell sorting; ss.
XX
OS Synthetic.
XX
FN WO9303172-A.
PD 18-FEB-1993.
XX
PF 31-JAN-1992; 92WO-US00801.
PR 01-AUG-1991; 91US-0739055.
XX
PA (UYRE-) UNIV RES CORP.
XX
PI Gold L, Prihnow D, Smith JD, Tuerc C;
DR WPI: 1993-076529/09.
XX
PT Systematic polypeptide evolution by reverse translation - used
PT for prodn. of polypeptide ligand specific for desired target
PT molecule
XX
XX Example 1; Page 84; 98pp; English.
XX
CC SPERT is used to select novel polypeptides that bind the antibody

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XX (GOLD/) GOLD L.  
 PA (TUER/) TUERK C.  
 PA (PRIB/) PRIBNOW D.  
 PA (SMIT/) SMITH J D.  
 XX  
 PI Gold L, Tuerk C, Pribnow D, Smith JD;  
 XX  
 DR WPI; 2002-329128/36.  
 XX  
 PT New methods (termed SPERT (Systematic Polypeptide Evolution by Reverse  
 PT Translation)) for selecting high-affinity polypeptide ligands that  
 PT specifically bind target molecules, e.g. proteins, carbohydrates,  
 PT toxins, drugs and receptors -  
 XX  
 XX  
 XX

Example 1; Page 21; 38pp; English.

CC The sequences given in A172769-81 are oligonucleotides which were used  
 CC to make mRNA encoding a candidate polypeptide, a 5' fixed sequence  
 CC composed of a T7 promoter sequence and a ribosome binding site which is  
 CC recognised by both prokaryotic and eukaryotic ribosomes, terminating in  
 CC a restriction endonuclease site. The resulting nucleic acid was used in  
 CC the method of the invention for preparing ligands of target molecules  
 CC in which mixtures of ribosome complexes or mRNA:circle-solid:polypeptide  
 CC copolymers (mrcs.pcs) are partitioned by affinity to the target and  
 CC amplified to create candidate mixtures enriched in ribosome complexes  
 CC or mrcs.pcs with an affinity to the target, are new. The methods are  
 CC termed SPERT (Systematic Polypeptide Evolution by Reverse Translation).  
 CC The SPERT methods are useful for isolating polypeptide ligands for  
 CC desired target molecules. The polypeptide products are useful for  
 CC any purpose to which a binding reaction may be put, for example in  
 CC assay methods, diagnostic procedures, cell sorting, as inhibitors of  
 CC target molecule function, as probes, as sequestering agents and the  
 CC like. In addition, polypeptide products of the invention can have  
 CC catalytic activity. Target molecules include natural and synthetic  
 CC polymers, including proteins, polysaccharides, glycoproteins, hormones,  
 CC receptors and cell surfaces, nucleic acids, and small molecules such as  
 CC drugs, metabolites, cofactors, transition state analogues and toxins.  
 CC The novel SPERT method involves utilizing a candidate mixture of  
 CC polypeptides having a randomized amino acid sequence. Each member of  
 CC the mixture is linked to an individualized mRNA, which encodes the  
 CC amino acid sequence of that polypeptide. The candidate polypeptides are  
 CC partitioned according to their property of binding to a given desired  
 CC target molecule. The partitioning is carried out in such a way that  
 CC each mRNA encoding a polypeptide is partitioned exactly together with  
 CC that polypeptide. In this way each polypeptide is partitioned together  
 CC with the means for further amplifying it by an in vitro process.  
 CC Ultimately, both the desired optimal polypeptide ligand of the desired  
 CC target and the mRNA encoding the polypeptide are simultaneously  
 CC selected, allowing further synthesis of the selected polypeptide as  
 CC desired, and further amplification of the coding sequence. It is  
 CC therefore not necessary to analyse the amino acid sequence of the  
 CC selected polypeptide (using protein chemistry) in order to produce it  
 CC in desired quantities.  
 XX  
 XX

SO Sequence 390 BP; 125 A; 126 C; 133 G; 6 T; 0 other;

Query Match Best Local Similarity 3.2%; Score 41.6; DB 24; Length 390;

Matches 95; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 1003 GAGCGAAGAAAGCAGGAGGCCCCCTCCAGAGACCTCGAGAGCGACATGCACAGCA 1062  
 DB 201 GAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 260  
 QY 1063 GAGGCTTCTGAGAAATCTGCGCCCTCCGGAAGACAGCAAGTCCCGAGAGACACC 1122  
 DB 261 GAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 320  
 QY 1123 GAGCAGCATATCCAACTCGGATCCTGACTATTACATGACATGCCGCGTGATCCG 1182  
 DB 321 GAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 380

QY 1183 GTGG 1186  
 DB 381 ATGG 384

#### RESULT 15

AAC44461  
 ID AAC44461 standard; DNA: 1761 BP.

AAC44461;

18-OCT-2000 (first entry)

Zea mays DNA fragment SEQ ID NO: 42909.

XX Hybridisation assay; genetic mapping; gene expression control;  
 KM protein identification; signal transduction pathway; metabolic;  
 KM pathway; promoter; termination sequence; corn; ss.

XX Zea mays subsp. mays.

PN EP1033405-A2.

PD 06-SEP-2000.

PE 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 28-APR-1999; 99US-0130891.

PR 30-APR-1999; 99US-0131449.

PR 30-APR-1999; 99US-0132048.

PR 04-MAY-1999; 99US-0132407.

PR 05-MAY-1999; 99US-0132484.

PR 06-MAY-1999; 99US-0132485.

PR 07-MAY-1999; 99US-0132487.

PR 11-MAY-1999; 99US-0132863.

PR 14-MAY-1999; 99US-0134218.

PR 14-MAY-1999; 99US-0134219.

PR 14-MAY-1999; 99US-0134321.

PR 18-MAY-1999; 99US-0134370.

PR 18-MAY-1999; 99US-0134768.

PR 19-MAY-1999; 99US-0134941.

PR 20-MAY-1999; 99US-0135124.

PR 21-MAY-1999; 99US-0135353.

PR 24-MAY-1999; 99US-0135629.

PR 25-MAY-1999; 99US-0136021.

PR 27-MAY-1999; 99US-0136392.

PR 28-MAY-1999; 99US-0136782.

PR 01-JUN-1999; 99US-0137222.

PR 03-JUN-1999; 99US-0137528.

PR 04-JUN-1999; 99US-0137502.

PR 07-JUN-1999; 99US-0137724.

PR 08-JUN-1999; 99US-0138094.

PR 10-JUN-1999; 99US-0138540.

PR 10-JUN-1999; 99US-0138847.

PR 14-JUN-1999; 99US-0139119.

PR 16-JUN-1999; 99US-0139452.

PR 16-JUN-1999; 99US-0139453.

PR 17-JUN-1999; 99US-0139492.

[illegible]

PR	16-AUG-1999;	9905-0149368
PR	17-AUG-1999;	9905-0149175
PR	18-AUG-1999;	9905-0149426
PR	20-AUG-1999;	9905-0149722
PR	20-AUG-1999;	9905-0149723
PR	22-AUG-1999;	9905-0149929
PR	23-AUG-1999;	9905-0149902
PR	23-AUG-1999;	9905-0149930
PR	25-AUG-1999;	9905-0150566
PR	26-AUG-1999;	9905-0150884
PR	27-AUG-1999;	9905-0151065
PR	27-AUG-1999;	9905-0151066
PR	27-AUG-1999;	9905-0151080
PR	30-AUG-1999;	9905-0151303
PR	31-AUG-1999;	9905-0151438
PR	01-SEP-1999;	9905-0151930
PR	07-SEP-1999;	9905-0152363
PR	10-SEP-1999;	9905-0153070
PR	13-SEP-1999;	9905-0153758
PR	15-SEP-1999;	9905-0154018
PR	16-SEP-1999;	9905-0154039
PR	20-SEP-1999;	9905-0154779
PR	22-SEP-1999;	9905-0155133
PR	23-SEP-1999;	9905-0155486
PR	24-SEP-1999;	9905-0155653
PR	28-SEP-1999;	9905-0156458
PR	29-SEP-1999;	9905-0156596
PR	04-OCT-1999;	9905-0157117
PR	05-OCT-1999;	9905-0157755
PR	06-OCT-1999;	9905-0157863
PR	07-OCT-1999;	9905-0158029
PR	08-OCT-1999;	9905-0158232
PR	12-OCT-1999;	9905-0158361
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PR	28-OCT-1999;	9905-0161920
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PR	29-OCT-1999;	9905-0161993
PR	29-OCT-1999;	9905-0162142

Query Match	2.9%	Score 38.4;	DB 21;	Length 1761;
Best Local Similarity	46.1%;	Pred. No. 0.27;		
Matches 129;	Conservative 0;	Mismatches 151;	Indels 0;	Gaps 0;

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Db	172	GACATCTCTGCTGCTCTTCTGCCGGGGCCAGCACTCCGTCCGCTCTCAAGGGCAATGT	231
QY	267	CAATTTAGCCGCTGCGCGCGCTCGACGCGCTAACCATACCGCGGTTGGCCCGTTAAACG	326
Db	232	CGTGTGCTCGTGGGGGACAGGGGCGAGACGGGCACTGCGGCACAGCGGCAGCGAGGACCG	291

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QY 327 ATACCTCAGTAGGCTATCAAGAGGCTGCGAGCTGTGAGCTCAACCCGATTCTAACGT 386
Db 292 GCTGTCGCCACAGGCTTACGAGGCTTCGAGCGCGCCGAGTCAAGTCAATCTGCGG 351
QY 387 GGACGACATGATATCGGCGGCCCAAGAAAGAGAGAGGGGGCCCTTCGAGGCCCTCCGT 446
Db 352 TCCGACACACACACCGCTACTCCGAGGACGAGCTGCAAGTCTACAGCTGGGGCTGGGG 411
QY 447 CGTCTGTTCTACGTGATTTAAGGGCGAGCGAGCGGCGAGGAC 486
Db 412 AGACTTCGGGAGGCTGGGGCATGGGAACCTCCAGCGAGCTC 451

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